



STIC Search Report

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STIC Database Tracking Number: 108672

TO: Manjunath N Rao
Location: CM1/10D01/10A11
Art Unit: 1652
Tuesday, November 25, 2003
Case Serial Number: 10/005306

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



STIC-Biotech/ChemLib

108670

From: Chan, Christina
Sent: Wednesday, November 19, 2003 3:32 PM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search request for 10/005,306

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Rao, Manjunath N.
Sent: Wednesday, November 19, 2003 2:48 PM
To: Chan, Christina
Subject: RUSH sequence search request for 10/005,306

Hello Christina,

Please authorize the request below as RUSH. The reason being this is an IFW due this bi-week.

From: Manjunath N. Rao
Art Unit 1652, Room 10A11
Mail Box in Room 10D 01
Phone: 306-5681

Date: 11-19-03

Please search the following as soon as possible for application with serial number

10/005306

1. SEQ ID NO: 9 against all commercial amino acid databases, issued patents/published applications database and pending application database. Please provide a print of all results.

If you have any questions please call me at the above phone number.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 11/21
Date Completed: 11/25
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Thanks

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Mail Box in 10D01
Crystal Mall 1, USPTO.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
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Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
| 1 | 100 | 100 | 1 | ... |

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|---|------|-------|-----|----|----------|--|
| 1 | 1367 | 100.0 | 260 | 19 | AMN95937 | Human mature DNase |
| 2 | 1364 | 99.8 | 260 | 19 | AMN95928 | Human mature DNase |
| 3 | 1364 | 99.8 | 260 | 19 | AMN95928 | Human mature DNase |
| 4 | 1362 | 99.6 | 260 | 19 | AMN94942 | Human mature DNase |
| 5 | 1362 | 99.6 | 260 | 19 | AMN95929 | Human mature DNase |
| 6 | 1362 | 99.6 | 260 | 23 | AMN15522 | Human DNase 1, Ho |
| 7 | 1362 | 99.6 | 262 | 15 | AMN5356 | Human DNase 1, Ho |
| 8 | 1362 | 99.6 | 262 | 15 | AMN5356 | Human DNase 1, Ho |
| 9 | 1362 | 99.6 | 283 | 24 | ABP96447 | Psychotic human brain presynaptic vesicles |

[illegible]

RESULT 1

AAW49937
ID AAW49937 standard: protein: 260 AA.

AAW49937;

05-JUN-1998 (first entry)

Human mature DNase T variant N74K.

XX Mature DNase T. variant: hyperactive

KW systemic lupus erythematosus; cyst
KW ashrma; tuberculosis

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ID AMW03666 standard; protein; 260 AA.
 AC AMW03666;
 XX 02-MAY-1997 (first entry)
 DT 02-MAY-1997 (first entry)
 DE Wild type human DNase I.
 XX human mature DNase I; actin-resistant variant; treat; pulmonary disease;
 KW human mature DNase I; actin-resistant variant; treat; pulmonary disease;
 KW consistency; asthma; systemic lupus erythematosus; in vitro; assay.
 XX Homo sapiens.
 OS Homo sapiens.
 PN W09626279-A1.
 XX 29-AUG-1996.
 PP 21-FEB-1996; 96MO-US02421.
 XX 10-OCT-1995; 95US-0540527.
 FR 24-FEB-1995; 95MO-US03366.
 XX (GETH) GENENTECH INC.
 PA Lazarus RA, Shuk S, Ulmer JS;
 XX WPI; 1996-402370/40.
 DR New actin-resistant human DNaseI variants, used for reducing the
 FT actin resistance of human DNaseI variants. E.g. for treating
 FT chronic bronchitis or cystic fibrosis
 XX Claim 4; Fig 1; 149pp; English.
 CC The present sequence is that of human mature DNase I. Actin-resistant
 CC variants of human DNase I (see AMW4323-421) are used to treat pulmonary
 CC diseases or disorders esp. cystic fibrosis or chronic bronchitis. They
 CC are used as a control in the treatment of chronic bronchitis or
 CC DNA-control material in a patient. They can be used for treating e.g.
 CC acute or chronic bronchial pulmonary disease, asthma, systemic lupus
 CC erythematosus. They can also be used in in vitro diagnostic assays of a
 CC chronic mutant human actin-resistant DNase I. Present and
 CC with an actin-resistant DNase I variant. An appropriate candidate for
 CC reduced affinity for actin, their DNA hydrolytic activity is less
 CC than that of wild type DNase I. The actin-resistant DNase I variant
 CC macrolytic activity in the presence of actin as compared to native human
 CC DNase I.
 XX Sequence 260 AA;
 CC
 CC Query Match 99.6%; Score 1362; DB 17; Length 260;
 CC Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 CC Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAFNIQTFSTGNSATVSYVQLSRDIALVQVDSHSLZAVKGLNMQDAP 60
 DB 1 LKIAFNIQTFSTGNSATVSYVQLSRDIALVQVDSHSLZAVKGLNMQDAP 60
 QY 61 DTVHVSSEFGKSKYKLYFVPPDQVSAVDSTYDQCEPCQNTFNPBPALVFPS 120
 DB 61 DTVHVSSEFGKSKYKLYFVPPDQVSAVDSTYDQCEPCQNTFNPBPALVFPS 120
 QY 121 RTFTEVFAVLPHAAAGDVAETDALVDYDLVQKGLDQVLMQDNAGCSYVPSO 180
 DB 121 RTFTEVFAVLPHAAAGDVAETDALVDYDLVQKGLDQVLMQDNAGCSYVPSO 180
 QY 181 WSRSLATPSTFQHLPGDATTPTTCACDRIYVAGMLNCAVQDPSALPFNFAAYO 240
 DB 181 WSRSLATPSTFQHLPGDATTPTTCACDRIYVAGMLNCAVQDPSALPFNFAAYO 240
 QY 241 LSDQAQALSDHPTVWVWLK 260

DB 241 LSDQAQALSDHPTVWVWLK 260
 RESULT 4
 ID AMW49942 standard; protein; 260 AA.
 AC AMW49942;
 XX AMW49942;
 DT 05-JUN-1998 (first entry)
 DE Human mature DNase I variant E13R.N74K.
 XX Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia;
 KW systemic lupus erythematosus; cystic fibrosis; bronchitis; emphysema;
 KW asthma; tuberculosis.
 XX Homo sapiens.
 OS Homo sapiens.
 PN Synthetic.
 XX Misc-difference 13 /Label= E13R
 XX /Note= "wild-type Glu is replaced by Arg"
 XX Misc-difference /Label= N74K
 XX /Note= "wild-type Asn is replaced by Lys"
 XX W09747751-A1.
 XX 18-DEC-1997.
 XX 09-JUN-1997; 97MO-US08517.
 XX 14-JUN-1996; 96US-0663831.
 XX (GETH) GENENTECH INC.
 XX Lazarus RA, Pan C;
 XX WPI; 1996-052315/05.
 XX Hyperactive variant of human DNaseI - useful to treat pulmonary
 XX disease, e.g. cystic fibrosis and systemic lupus erythematosus
 XX
 XX Disclosure; Pages 30-31; 46pp; English.
 CC This is an hyperactive variant of the human mature DNase I. This double
 CC mutant is created by substitutions of wild-type amino acids Glu and Asn
 CC at positions 13 and 74, respectively. The variant is useful to treat
 CC diseases by Arg and Lys residues. The variant is useful to treat
 CC systemic lupus erythematosus, bronchitis, pneumonia, emphysema, asthma
 CC and tuberculosis, where it reduces the viscoelasticity of pulmonary
 CC secretions. It can be used as an adjunct in the treatment of
 CC treatment of infectious lesions of the skin and mucosa and burns, where
 CC it may improve the activity of antibiotics. The variant can also be used
 CC to reduce and prevent the formation of DNA containing immune complexes in
 CC the treatment of autoimmune diseases. The variant can also be used to
 CC measure the variant in clinical samples, and when immobilised, to purify
 CC it from recombinant cell cultures. Compared with wild type enzyme, the
 CC hyperactive variant has a greater mucolytic activity and is more
 CC effective in degrading DNA generally. It is less sensitive to inhibition
 CC by NaCl, so it is more active under physiological conditions.
 XX Sequence 260 AA;
 CC
 CC Query Match 99.6%; Score 1362; DB 19; Length 260;
 CC Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 CC Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAFNIQTFSTGNSATVSYVQLSRDIALVQVDSHSLZAVKGLNMQDAP 60

XX 28-FEB-2001; 2001US-0796774.
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 PR 10-OCT-1995; 95US-0540527.
 PR 15-SEP-1997; 97US-0529995.
 PR 24-FEB-1995; 95NO-US02166.
 PR 24-MAR-1996; 96US-0403873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Lazarus RA, Shak S, Ulmer JS;
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 XX WPI; 2002-017217/02.
 DR
 XX
 XX Actin-resistant variants of human Dnaase I and chronic bronchitis,
 XX useful for treating cystic fibrosis and chronic bronchitis -
 XX
 XX Claim 4; Fig 1; 25pp; English.
 XX
 XX The invention relates to human Dnaase I actin-resistant variants and
 XX the nucleic acids that encode them. The variants are useful in the
 XX treatment of cystic fibrosis and chronic bronchitis, pneumonia,
 XX bronchiectasis, emphysema, asthma, and systemic lupus erythematosus.
 XX Dnaase I reduces the viscoelasticity of pulmonary secretions (mucus) in
 XX cystic fibrosis and chronic bronchitis. The variants of Dnaase I are
 XX clearing of respiratory airways. In the presence of actin, adding in the
 XX DNA-hydrolytic activity of Dnaase I is inhibited. Actin-resistant Dnaase I
 XX variants have decreased ability to bind actin, but still have mucolytic
 XX activity. The variants of Dnaase I are useful in the treatment of cystic
 XX to native human Dnaase I because their DNA-hydrolytic activity is
 XX less inhibited. The present sequence is native human Dnaase I.
 XX
 XX Sequence 260 aa;
 Query Match 99.6%; Score 1362; DB 23; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKTAAPNITGTGETMSNATLVSYVQLSRDYALVQVRDHSHTLVGKLLNDQAP 60
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 QY 61 DTVHVVSPVPLGRSKYKRLVYVPRDQVSAVSYVYDDGCPGQNDTFNRPATVRFSS 120
 DB 61 DTVHVVSPVPLGRSKYKRLVYVPRDQVSAVSYVYDDGCPGQNDTFNRPATVRFSS 120
 QY 121 RFTVEFEPAIVPLAAPDAVAEIDALYDVLVQEKNGLEDVLMGDFNAGCSYVRFSSQ 180
 DB 121 RFTVEFEPAIVPLAAPDAVAEIDALYDVLVQEKNGLEDVLMGDFNAGCSYVRFSSQ 180
 QY 181 WSSRLWSTPTQWLIPDSAUTTPTPHCAVDRIVAGMLLGAIVPDSALPFFNQAVG 240
 DB 181 WSSRLWSTPTQWLIPDSAUTTPTPHCAVDRIVAGMLLGAIVPDSALPFFNQAVG 240
 QY 241 LSDQLAQISDHPVEWLK 260
 DB 241 LSDQLAQISDHPVEWLK 260
 RESULT 7
 AAR45356
 ID AAR45356 standard; Protein; 282 AA.
 AC AAR45356;
 XX
 XX 25-MAR-2003 (updated)
 DT 22-JUN-1994 (first entry)
 DR
 XX Human Dnaase I.
 XX
 XX Dnaase; non-deamidated; deamidated; pulmonary distress;
 XX cystic fibrosis; chronic bronchitis; emphysema; pneumonia;
 XX asthma, tuberculosis; fungal infection.

XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..22
 XX Protein /label= sig_peptide
 XX /label= mat_protein
 XX
 XX W03235670-A1.
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 XX 28-DEC-1993.
 XX
 XX 28-MAY-1993; 93WO-US05136.
 XX
 XX 08-JUN-1992; 92US-0895300.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Frenz J, Shire SJ, Sliwkowski MB;
 XX WPI; 1994-007128/01.
 XX N-PSDB; AAQ34429.
 XX
 XX Purified forms of non-deamidated and deamidated human Dnaase - for
 XX treatment of pulmonary distress, cystic fibrosis, chronic
 XX bronchitis, emphysema, pneumonia, asthma, tuberculosis and fungal
 XX infections
 XX
 XX Disclosure; Fig 1; 38pp; English.
 XX
 XX Two components of a recombinant prepn. of Dnaase are identified and
 XX characterised. A separation method and uses of these components
 XX are given in the specification.
 XX CC (updated on 25-MAR-2003 to correct EN field.)
 CC
 CC Sequence 282 AA;
 QY Query Match 99.6%; Score 1362; DB 15; Length 282;
 Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKTAAPNITGTGETMSNATLVSYVQLSRDYALVQVRDHSHTLVGKLLNDQAP 60
 DB 23 LKTAAPNITGTGETMSNATLVSYVQLSRDYALVQVRDHSHTLVGKLLNDQAP 60
 QY 61 DTVHVVSPVPLGRSKYKRLVYVPRDQVSAVSYVYDDGCPGQNDTFNRPATVRFSS 120
 DB 61 DTVHVVSPVPLGRSKYKRLVYVPRDQVSAVSYVYDDGCPGQNDTFNRPATVRFSS 120
 QY 121 RFTVEFEPAIVPLAAPDAVAEIDALYDVLVQEKNGLEDVLMGDFNAGCSYVRFSSQ 180
 DB 143 RFTVEFEPAIVPLAAPDAVAEIDALYDVLVQEKNGLEDVLMGDFNAGCSYVRFSSQ 202
 QY 181 WSSRLWSTPTQWLIPDSAUTTPTPHCAVDRIVAGMLLGAIVPDSALPFFNQAVG 240
 DB 203 WSSRLWSTPTQWLIPDSAUTTPTPHCAVDRIVAGMLLGAIVPDSALPFFNQAVG 262
 QY 241 LSDQLAQISDHPVEWLK 260
 DB 263 LSDQLAQISDHPVEWLK 282
 RESULT 8
 AAM52142
 ID AAM52142 standard; Protein; 282 AA.
 AC AAM52142;
 XX
 XX 05-FEB-2002 (first entry)
 DT
 XX Human Dnaase I encoding polynucleotide 1.
 XX
 XX

KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
KW

| | |
|----|------------------------------|
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WC200174905-AL. |
| XX | |
| PD | 11-OCT-2001. |
| XX | |
| PA | 26-MAR-2001, 2001NC-GB01324. |
| XX | |
| PR | 03-APR-2000; 2000GB-0008049. |
| PR | 02-OCT-2000; 2000US-237159F. |
| PA | (ANTI-) ANTISOMA RES LTD. |

Young RJ;
WPI: 2001-662969/76.
Novel compounds used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymeric epithelial mucin, and cytotoxic portion having endonucleolytic activity -
Disclosure: Figure 1, 176pp, English.
The invention relates to a compound which comprises a target cell binding portion and a cytotoxic portion. The target cell binding portion has specificity for polymeric epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AM52254-AM52168 and encoded by ABA05682-ABA03728. The compound is useful for treating cancer and acting as a potential inducer of apoptosis.

| Seq | Sequence | 282 AA ₁ | Query Match | Best Local Similarity | 99.6%; Score 1362; DB 282; Pred. No. 1.1e-146; Matrix 255; Conservative | 0; Mismatch 1; Indels 0; Gaps 0; |
|-----|----------|--|-------------|-----------------------|---|----------------------------------|
| QY | 1 | LKIAENRQIFQFTGNSGNATSYIVQLISRTDIALVQEVDSHGTHAGKLLNDQAP | 60 | 60 | 60 | 60 |
| DD | 23 | LKIAENRQIFQFTGNSGNATSYIVQLISRTDIALVQEVDSHGTHAGKLLNDQAP | 82 | 82 | 82 | 82 |
| QY | 61 | DTYVHWSEFAGKSTKERYLFPYRDPQNSVSYTDDGCEGNDNFRPEALVFES | 120 | 120 | 120 | 120 |
| DD | 83 | DTYVHWSEFAGKSTKERYLFPYRDPQNSVSYTDDGCEGNDNFRPEALVFES | 142 | 142 | 142 | 142 |
| QY | 121 | RFTVEFEALVFLHAARGDAFAIDALDYVLVDQVKGSLDWDMGDFNACGCVTFV | 180 | 180 | 180 | 180 |
| DD | 143 | RFTVEFEALVFLHAARGDAFAIDALDYVLVDQVKGSLDWDMGDFNACGCVTFV | 202 | 202 | 202 | 202 |
| QY | 181 | WSEIRLWTSFQFQMLPDSARITTTTCPCIVIRIVLQGLKGVAVPDSALFNQAAV | 240 | 240 | 240 | 240 |
| DD | 203 | WSEIRLWTSFQFQMLPDSARITTTTCPCIVIRIVLQGLKGVAVPDSALFNQAAV | 262 | 262 | 262 | 262 |
| QY | 241 | LSQSLQAKQTSREHWEMK | 260 | 260 | 260 | 260 |
| DD | 263 | LSQSLQAKQTSREHWEMK | 282 | 282 | 282 | 282 |

| | |
|----------|--|
| RESULT 9 | |
| ABP96647 | |
| CD | ABP96647 standard; Protein; 282 AA. |
| XX | |
| AC | ABP96647; |
| XX | |
| XX | 30-MAY-2003 (first entry) |
| XX | Deoxyribonuclease I protein SEQ ID NO:3. |
| XX | Deoxyribonuclease I protein |
| XX | Deoxyribonuclease I; DNase-I; deoxyribonuclease; enzyme; |
| XX | |

| | |
|----|---|
| XX | respiratory system disease. |
| XX | Unidentified. |
| XX | CN136602-A. |
| XX | |
| XX | 28-AUG-2002. |
| XX | |
| XX | 19-JAN-2001; 2001CN-0101653. |
| XX | |
| XX | 19-JAN-2001; 2001CN-0101653. |
| XX | |
| XX | (HUAD-) HUADA GENE RES CENT BEIJING. |
| XX | |
| XX | Liu S, Feng X, Wang C; |
| XX | WFI; 2003-240395/24. |
| XX | N-PSDB; ACC4559. |
| XX | |
| XX | Process for preparing recombinant deoxyribonuclease I - |
| XX | Example 1, Page 18-19 (disclosure); 23DP; Chinese. |
| XX | |

[illegible][illegible]


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XX 11-OCT-2001.
XX 26-MAR-2001; 2001KO-GB01324.
XX 03-APR-2000; 2000GB-0008049.
XX 02-OCT-2000; 2000US-237159P.
XX (AMTI-) ANTISOMA RES LTD.
XX Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity -
XX Claim 20; Figure 17; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AMS2155-AM52156 and encoded by AA02682-AA02738. The
XX compound has cytotoxic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 525 AA;
XX Query Match 99.6%; Score 1362; DB 22; Length 525;
XX Best Local Similarity 99.6%; Pred. No. 3.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 60
DB 256 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 315
OY 61 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 120
DB 316 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 375
OY 121 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 180
DB 376 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 435
OY 181 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 240
DB 436 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 495
XX Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity -
XX Claim 20; Figure 17; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AMS2155-AM52156 and encoded by AA02682-AA02738. The
XX compound has cytotoxic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 525 AA;
XX Query Match 99.6%; Score 1362; DB 22; Length 525;
XX Best Local Similarity 99.6%; Pred. No. 3.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 60
DB 256 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 315
OY 61 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 120
DB 316 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 375
OY 121 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 180
DB 376 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 435
OY 181 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 240
DB 436 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 495
XX Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity -
XX Claim 20; Figure 6; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AMS2155-AM52156 and encoded by AA02682-AA02738. The
XX compound has cytotoxic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 527 AB;
XX Query Match 99.6%; Score 1362; DB 22; Length 527;
XX Best Local Similarity 99.6%; Pred. No. 3.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 60
DB 258 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 317
OY 61 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 120
DB 318 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 377
OY 121 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 180
DB 378 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 437
OY 181 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 240
DB 438 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 497
XX Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity -
XX Claim 20; Figure 6; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AMS2155-AM52156 and encoded by AA02682-AA02738. The
XX compound has cytotoxic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 527 AB;
XX Query Match 99.6%; Score 1362; DB 22; Length 527;
XX Best Local Similarity 99.6%; Pred. No. 3.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 60
DB 258 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 317
OY 61 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 120
DB 318 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 377
OY 121 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 180
DB 378 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 437
OY 181 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 240
DB 438 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 497
XX Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity -
XX Claim 20; Figure 6; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AMS2155-AM52156 and encoded by AA02682-AA02738. The
XX compound has cytotoxic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 527 AB;
XX Query Match 99.6%; Score 1362; DB 22; Length 527;
XX Best Local Similarity 99.6%; Pred. No. 3.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 60
DB 258 LKTAARNICFTGCTGASNATLVSYVQILSRVYDALVQVESHSLTAVGKLLDNLDAP 317
OY 61 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 120
DB 318 DTVHWVSEPLGRSKYERYLFPYRPODVSVDYDCCPCGCDTFRNEPAIVRFS 377
OY 121 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 180
DB 378 RFTVREFAIVPLAAFGQVAIDVLDVLDVQVKGLEWMLGDFNAGCSYVRPQ 437
OY 181 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 240
DB 438 WSTRILWTSPTQMLPDSADTTATPTFHCADRIIVAGNLLGAVVDSALPFPQAA 497

```

Search completed; November 21, 2003, 13:55:10
Job time : 42 secg

DB 83 DTYHYVSEPLGRNSYKERYLTFVYKFDQVSAVDSYYDDGCEPCGNDTFNKEPALVRFFS 142

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Db 143 RPTVEPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 202
 QY 181 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 240
 Db 203 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 262
 QY 241 LSQDLQAALSDHPFVEMVK 260
 Db 263 LSQDLQAALSDHPFVEMVK 282

RESULT 2
 deoxyribonuclease I (EC 3.1.21.1) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: J13876
 C:Keywords: hydrolase
 Nucleic Acids Res. 18, 7151, 1990
 A:Title: Nucleotide sequence of a full length cDNA clone encoding the deoxyribonuclease
 A:Reference number: J13876; MUID:9108912; PMID:2263485
 A:Cross-references: ENBL:X56040
 A:Molecule type: mRNA
 A:Residues: 1-284 <POL>
 A:Superfamily: deoxyribonuclease I
 C:Keywords: hydrolase

Query Match 82.6%; Score 1129; DB 1: Length 284;
 Best Local Similarity 80.4%; Seq. Id. 96; 22; Indels 0; Gaps 0;
 Matches 209; Conservative 29; Mismatches 22; Indels 0; Gaps 0;

QY 1 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 60
 Db 23 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 82
 QY 61 DTYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 120
 Db 83 DTRYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 142
 QY 121 RPTVEPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 180
 Db 143 PTVREPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 202
 QY 181 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 240
 Db 203 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 262
 QY 241 LSQDLQAALSDHPFVEMVK 260
 Db 263 LTNQAGALSDHPFVETLIR 282

RESULT 3
 deoxyribonuclease I (EC 3.1.21.1) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: J02526
 C:Keywords: hydrolase
 J. Peitsch, M.C.; Imbler, M.; French, J.E.; Tschopp, J.
 A:Title: Genomic organization and expression of mouse deoxyribonuclease I.
 A:Reference number: J02526; MUID:95160718; PMID:7857306
 A:Cross-references: ENBL:U00478; NID:9437052; PID:AA03710.1; PID:9437053
 A:Residues: 1-284 <PRE>
 A:Superfamily: deoxyribonuclease I
 C:Keywords: actin binding; calcium binding; hydrolase

Query Match 82.4%; Score 1127; DB 1: Length 284;
 Best Local Similarity 81.5%; Pred. No. 4.6e-96;

Matches 212; Conservative 23; Mismatches 25; Indels 0; Gaps 0;
 QY 1 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 60
 Db 23 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 82
 QY 61 DTYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 120
 Db 83 DTRYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 142
 QY 121 RPTVEPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 180
 Db 143 PTVREPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 202
 QY 181 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 240
 Db 203 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 262
 QY 241 LSQDLQAALSDHPFVEMVK 260
 Db 263 LSNQAGALSDHPFVETLIR 282

RESULT 4
 deoxyribonuclease I (EC 3.1.21.1) - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A26324
 R. Paudel, H.K.; Liao, T.H.
 J. Biol. Chem. 261, 16006-16011, 1986
 A:Title: Isolation and characterization of the complete amino acid sequence of porcine
 A:Reference number: A26324; MUID:8705260; PMID:782104
 A:Cross-references: ENBL:X56040
 A:Molecule type: protein
 A:Residues: 1-284 <PRE>
 A:Superfamily: deoxyribonuclease I
 C:Keywords: hydrolase

Query Match 78.4%; Score 1072; DB 1: Length 262;
 Best Local Similarity 77.3%; Seq. Id. 93; 21; Indels 0; Gaps 0;
 Matches 201; Conservative 30; Mismatches 29; Indels 0; Gaps 0;

QY 1 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 60
 Db 23 LKTAAPNIOGTGNTSNATLVSYVQLSRDYALVQVRSHTAVGKLLMDLNAQAP 82
 QY 61 DTYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 120
 Db 83 DTRYHYVSEPLGRSKYKRTLVPRDPQVAVDSYTDGCEPCONDFTNRPFAVRFSS 142
 QY 121 RPTVEPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 180
 Db 143 PTVREPEPAIVPLHAPGDAVAETDALVYLVQVQKGLDVLMDGDFNAGSVYRFSQ 202
 QY 181 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 240
 Db 203 NSRIKMTSPFQWLIPDSATATPTTCNDIVRIYVAGMLGRVAVPSALPFPQAAG 262
 QY 241 LSQDLQAALSDHPFVEMVK 260
 Db 241 LSGEPLALISDHPFVETLIR 260

RESULT 5
 deoxyribonuclease I (EC 3.1.21.1) precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 24-Apr-1984 #sequence_revision 05-Dec-1998 #text_change 16-Jun-2000
 C:Accession: J06533; A92133; A92134; A92148; A26325; A00782; S19525
 C:Keywords: hydrolase
 J. Chen, C. Lai, S. S. Liao, T.H. Liao, T.H.
 Gene 206, 181-194, 1996
 A:Title: Cloning, sequencing and expression of a cDNA encoding bovine pancreatic deoxy

Biochem. Biophys. Res. Commun. 231, 499-504, 1997
 A>Title: Cloning and characterization of a novel human DNase.
 A'Reference number: JC3561; MUID:97223487; PMID:9070308

A'Accession: JC3561

A'Keywords: DNase

A'Residuals: 1-305 <2EN>

C'Superfamily: deoxyribonuclease I

C'Keywords: hydrolase

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

181 SNLRLTVPQFQQLTPSADPTA--TFPHCAVRIYVQKLLAGVVDGALPFPN 239

195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 9

755251

Probable extracellular nuclease - Deinococcus radiodurans (strain R1)

C'Species: Deinococcus radiodurans

C'Date: 03-Dec-1999 Sequence revision 03-Dec-1999 #ext_change 31-Mar-2000

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

181 SNLRLTVPQFQQLTPSADPTA--TFPHCAVRIYVQKLLAGVVDGALPFPN 239

195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 8

755251

Probable extracellular nuclease (EC 3.1.-.-) - human

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

181 SNLRLTVPQFQQLTPSADPTA--TFPHCAVRIYVQKLLAGVVDGALPFPN 239

195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 8

755251

Probable extracellular nuclease (EC 3.1.-.-) - human

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

Biochem. Biophys. Res. Commun. 231, 499-504, 1997
 A>Title: Cloning and characterization of a novel human DNase.
 A'Reference number: JC3561; MUID:97223487; PMID:9070308

A'Accession: JC3561

A'Keywords: DNase

A'Residuals: 1-305 <2EN>

C'Superfamily: deoxyribonuclease I

C'Keywords: hydrolase

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

181 SNLRLTVPQFQQLTPSADPTA--TFPHCAVRIYVQKLLAGVVDGALPFPN 239

195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 9

755251

Probable extracellular nuclease - Deinococcus radiodurans (strain R1)

C'Species: Deinococcus radiodurans

C'Date: 03-Dec-1999 Sequence revision 03-Dec-1999 #ext_change 31-Mar-2000

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

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Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

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61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

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195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 8

755251

Probable extracellular nuclease (EC 3.1.-.-) - human

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

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61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

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240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 8

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Probable extracellular nuclease (EC 3.1.-.-) - human

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

Biochem. Biophys. Res. Commun. 231, 499-504, 1997
 A>Title: Cloning and characterization of a novel human DNase.
 A'Reference number: JC3561; MUID:97223487; PMID:9070308

A'Accession: JC3561

A'Keywords: DNase

A'Residuals: 1-305 <2EN>

C'Superfamily: deoxyribonuclease I

C'Keywords: hydrolase

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

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240 GSDGLQALQSHVYFVEMLK 260

253 QUTEEALNSINHYFVEMLK 273

RESULT 9

755251

Probable extracellular nuclease - Deinococcus radiodurans (strain R1)

C'Species: Deinococcus radiodurans

C'Date: 03-Dec-1999 Sequence revision 03-Dec-1999 #ext_change 31-Mar-2000

C'Accession: J01517

C'Keywords: nuclease

F121-305/Predicted: deoxyribonuclease I

F155/Active site: His #status predicted

Query Match

Similarity 42.24; Score 591; DB 2; Length 305;

Matches 119; Conservative 51; Mismatches 489; Indels 4; Gaps 3;

1 LKTAAPNQTFTSTNSNATLNSVTLVSFDIALVQVSRSHLTAVGKLLDNLGAP 60

20 RICHVNAQLVLRGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 79

61 DTVYVNSVPLGKRYEYVLPVPRQNSAVSYVYDGCCEGQGNTPRPAVRF 120

80 GFVSTLASQLGRESTMETVYVFRSHKTVLASVYVND-----EDVFAPEFPV 134

121 AFTVEFPALVPLARQDAVDALVDVLYQVQKSEKLEKLVQKSPGNSCSYVR 180

135 PSNVPLSLVPLVPLTPFAVEKELNALVDVLEVSQHQMSQVLLGDFNACAS 194

181 SNLRLTVPQFQQLTPSADPTA--TFPHCAVRIYVQKLLAGVVDGALPFPN 239

195 LQGLKELATPEFPIVAGDGEVTVRASTHCTYDVRVLKRECRSL--HTAA 252

A:Accession: J01157
A:Molecule type: genomic RNA
A:Residues: 1-1646 <GB>
A:Cross-references: GB:D12505
C:Superfamily: cucumber mosaic virus RNA 1 protein

Query Match 74%; Score 100.5; DB 1; Length 1646;
Best Local Similarity 22.9%; Pred. No. 1.5;
Matches 56; Conservative 37; Mismatches 81; Indels 71; Gaps 14;

QY 46 TANGKLLDNADAP-DTY-HVVVSEPLGR-----KSYKXYLYVYRPDQVSA----- 91
| | | | |
DQ 131 SAGVGLANFNFDYFATPTVYHMKYKQKPKRDTSTGSEYFALQTVTHPKVNVVGFV 137
| | | | |
QY 922 -----VDS-----VYVDGCEPCGNUTNREPAIVFRSEFTEVREPAIVPAHPA 1370
| | | | |
DQ 1371 FKYLTTFKLSWDSKSAFFY-----THKSPEDLQFFDSSHSDEYVLELDVSK 1420
| | | | |
QY 138 GDAVRAETDALAYDLVQWEGKGLDYN-----LWEDFNAGCS-----VYRPSQMS 1482
| | | | |
QY 1421 YDK-QQSDPSTFEMATWEKLGLODILANWMSGHKRTILQDPQAGIKTVLYQKRS--G 1477
| | | | |
QY 1483 SIKATKSTPFF-----QWGLPDSATPTATGVNVDVYHIVQKGLKRAVVD-----SALP 232
| | | | |
DQ 1478 DVTTTGTFTTIAACVASNLPL-LDKCFKPSACDDSLI-----VLPKGLRYPDIOANTLV 1532
| | | | |
QY 233 FNQQA 237
| | | | |
DQ 1533 NNTFA 1537

Result 11
T1132
T1133

nuclease - Aeromonas hydrophila
C:Species: Aeromonas hydrophila
C:Date: 22-Oct-1995 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
F:DoD: H. N. Robertson, J. M.
F:DoD: H. N. Robertson, J. M.
A:Article: Cloning, sequencing, and characterization of the nucleic gene encoding an extracellular nuclease from *Aeromonas hydrophila*.
A:Reference number: 120599; PMID:96272269; PMID:9662779
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1070 <DDB>
C:Cross-references: EMBL:L74304; NID:g1185048; PTD:g1185048; PTD:AMB59273.1
C:Genetic: A
C:Name: A

[illegible]

250 snrnp 254
DB 714 TDDP 718

RESULT 12

pre-mRNA splicing helicase BR22 - yeast (*Saccharomyces cerevisiae*)
Alternate names: DNA repair protein RAD24; protein YER172C
Accession: S50675; J03856; J04657
Date: 28-May-1993 sequence revision 24-Feb-1995 text_change 23-Mar-2001
R Dietrich, F.S. EMBL Data Library, December 1994
Description: The sequence of an S. cerevisiae coidms 9163 and 9132.
A:Accession: S50431
A:Accession: S50675
A:Molecule type: DNA
A:Cross-references: EMBL
A:Cross-references: XREF
R Mulligan, J.T. Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Taylor, J.
submitted to the EMBL Data library, February 1993
A:Accession: S50812
A:Accession: S50856
A:Molecule type: DNA
A:Residues: 1-169 <MUL>
A:Cross-references: EMBL:U11229
A:Cross-references: SGI:S0000974; MIPS:YER172C
Chinese Biochem J. 1:541-550, 1995
A:Title: Molecular cloning and sequencing of DNA repair gene RAD24.
A:Reference number: J04657
A:Accession: J04657
A:Accession: S50833
A:Residues: 1-260, "HCQT", 262, "XT", 265 <ZHU>
C:Genetics:
A:Gene: SGI:BR22; RAD24
A:Cross-references: SGI:S0000974; MIPS:YER172C
A:Cross-references: XREF
C:Supp. data: XREF DNA repair; nucleotide binding; nucleus; P-loop; pre-mRNA splicing
F630-632/Region: nucleotide-binding motif A (P-loop)
F630-635/Region: nucleotide-binding motif B
F634-637/Region: DEXH motif

Query Match
Best Local Similarity 24.8%; Pred. No. 9.5;
Matches 69; Conservative 30; Mismatches 86; Gaps 16;
6.8%; Score 93.5; DB 2; Length 2163;

10 TGE---TMSNTSLTVSVTLGSLVAVLQVDFSHSTAYVGLDNNV-----56

| | | | | | | |
|----|------|-----------------|------------------|-----------------|-----------------|------|
| Db | 882 | TFGRIIIITQGN--- | ---VYIYSVLQ--- | ---QPTSEQ--- | VSFKVDNNAWAGNIK | 930 |
| Qy | 57 | --QADP--- | THYV--VSEPGRK--- | | SYKSKFLPV-- | 84 |
| Db | 934 | CRDVAWMLAYITVYV | MLASPMCKVPD | ISDQKQKFSFLVSHS | ALCIQLKQELVLD | 990 |
| Qy | 85 | REQVDSAV--- | SVYIDQSCPGD | TFNNE--- | PALVPS--- | 120 |
| Db | 991 | AENVDTEATOLANT | ASSFVIH--- | ---ASMDVNRLED | DSHTTIGDILF | 1046 |
| Qy | 121 | RTFVRF--- | ALVPLHAPQDA | VEIDALVYLDVQ--- | EWKGEDVMLKGFNAG | 172 |
| Db | 1047 | RYEKREKLQLEAP | IPISRD | IPQAKVNLQVS | QLKFSFALSDITF | 1106 |
| Qy | 173 | CSYVRPSQMSRIWT | SPTFWL-- | IPDASDATATPHC | 209 | |
| Db | 1107 | RLLRAPFCICLRG | HGHFTMLNCKSNT | ITQSPFNC | 1144 | |

100

[illegible][illegible]

QY 1 LKAAANNITPFGTQNSATLNYVVOILSRVDTALVGVVSHSLAVKGLDNLNDAP 60
 DB 21 LKAAANNITPFGTQNSATLNYVVOILSRVDTALVGVVSHSLAVKGLDNLNDAP 62
 QY 61 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 120
 DB 121 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 120
 QY 83 NTYHVVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 142
 DB 121 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 142
 QY 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 DB 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 QY 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 DB 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 QY 181 NSIRLMTSPFQMLIPDSADTATPTHCADRVVAGLNGVAFVPSALPFPQANG 240
 DB 181 NSIRLMTSPFQMLIPDSADTATPTHCADRVVAGLNGVAFVPSALPFPQANG 240
 QY 241 LSQDLQAQLSHVPEVNL 259
 DB 241 LSQDLQAQLSHVPEVNL 259
 QY 241 LSQDLQAQLSHVPEVNL 259
 DB 241 LSQDLQAQLSHVPEVNL 259

RESULT 8
 DR1L CHECK STANDARD; PRT; 260 AA.
 ID AC P11377, 1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Deoxyribonuclease I (EC 3.1.21.1) (Dnaase I).
 OS Ovis aries (Sheep).
 CC Ovis aries; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mamalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Caprinae; Capriini; Caprinae; Ovis.
 RN NCBI_000000000: Ovis.
 [1] _transcript_

SEQUENCE
 RA MEDLINE:47057261; PubMed:3782105;
 RA Faidt H.K., Liao T.-H.;
 RA "Comparison of the three primary structures of deoxyribonuclease
 RA isolated from bovine, sheep, and chicken. The bovine and sheep
 RA published amino acid sequence of bovine Dnaase.";
 RA J. Biol. Chem. 261:16012-16017(1986).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC 3'-phosphonucleotide and 5'-phosphonucleotide end-products.
 CC -1- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZMOGEN
 CC GRANULES AND FOUND IN THE NUCLEAR ENVELOPE.
 CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC HSP; P00639; DNase I.
 DR InterPro; IPR001592; Dnaase I.
 DR InterPro; IPR005135; Eco_end_phos.
 DR PANTHER; P00639; DNase I.
 DR PRINTS; PR00130; DNaseI_1;
 DR ProDom; PD005408; Dnaase_I_N; 1.
 DR SMART; SM00476; DnaaseI_1; 1.
 DR PROSITE; PS00918; DNASE_I_2; 1.
 KM PROSITE; PS00918; DNASE_I_2; 1.
 KM DnaaseI; Endonuclease; Nuclease; Glycoprotein; Calcium;
 KM Apoptosis; Actin-binding.
 DR Apoptosis; Actin-binding.
 FT Dnaase I; 173 209 BY SIMILARITY
 FT ESSENTIAL FOR ENZYMIC ACTIVITY
 FT (BY SIMILARITY).
 FT ACT SITE 78 78 (BY SIMILARITY).
 FT RESIDUE 134 134 (BY SIMILARITY).
 FT CARGEND 16 16 N-LINKED (GLYCOC. .).

QY 1 LKAAANNITPFGTQNSATLNYVVOILSRVDTALVGVVSHSLAVKGLDNLNDAP 60
 DB 21 LKAAANNITPFGTQNSATLNYVVOILSRVDTALVGVVSHSLAVKGLDNLNDAP 62
 QY 61 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 120
 DB 121 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 120
 QY 83 NTYHVVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 142
 DB 121 DTHVWVSEPLGKSTKXERLVFVPEQVSNVYVYDGGECNCTVPEPALVAFS 142
 QY 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 DB 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 QY 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 DB 121 RFEVREFAVPLHARQVADLAVYLVGVVSHSLAVKGLDNLNDAP 180
 QY 181 NSIRLMTSPFQMLIPDSADTATPTHCADRVVAGLNGVAFVPSALPFPQANG 240
 DB 181 NSIRLMTSPFQMLIPDSADTATPTHCADRVVAGLNGVAFVPSALPFPQANG 240
 QY 241 LSQDLQAQLSHVPEVNL 259
 DB 241 LSQDLQAQLSHVPEVNL 259
 QY 241 LSQDLQAQLSHVPEVNL 259
 DB 241 LSQDLQAQLSHVPEVNL 259

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 CC Mamalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Caprinae; Capriini; Caprinae; Ovis.
 RN NCBI_000000000: Ovis.
 [1] _transcript_

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 RA Faidt H.K., Liao T.-H.;
 RA "Comparison of the three primary structures of deoxyribonuclease
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 CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC HSP; P00639; DNase I.
 DR InterPro; IPR001592; Dnaase I.
 DR InterPro; IPR005135; Eco_end_phos.
 DR PANTHER; P00639; DNase I.
 DR PRINTS; PR00130; DNaseI_1;
 DR ProDom; PD005408; Dnaase_I_N; 1.
 DR SMART; SM00476; DnaaseI_1; 1.
 DR PROSITE; PS00918; DNASE_I_2; 1.
 KM PROSITE; PS00918; DNASE_I_2; 1.
 KM DnaaseI; Endonuclease; Nuclease; Glycoprotein; Calcium;
 KM Apoptosis; Actin-binding.
 DR Apoptosis; Actin-binding.
 FT Dnaase I; 173 209 BY SIMILARITY
 FT ESSENTIAL FOR ENZYMIC ACTIVITY
 FT (BY SIMILARITY).
 FT ACT SITE 78 78 (BY SIMILARITY).
 FT RESIDUE 134 134 (BY SIMILARITY).
 FT CARGEND 16 16 N-LINKED (GLYCOC. .).


```

SEQUENCE FROM N.A.
RA De Maria A.B.; Arruti C.; deoxyribonuclease I.*;
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528509; AA93248.1; -.
DR InterPro; IPR001582; DNase_I.
DR Pfam; PF03370; Exo_endo_Phos.
DR PRINTS; PF00110; DNaseI.
DR ProDom; PD004508; DNase_I_1.
DR SMART; SM001582; DNaseI_1.
DR PROSITE; PS00919; DNase_I_1.
DR PROSITE; PS00918; DNase_I_2.
DR Signal; Hydrolase.
FT SIGNAL; Hydrolase.
SQ SEQUENCE 282 AA; 31331 MW; 43555HSLGCG0708E2 CRC64;

Query Match 77.8%; Score 1064; DB 6; Length 282;
Best Local Similarity 77.8%; Pred. No. 84e-96;
Matches 201; Conservative 28; Mismatches 30; Indels 0; Gaps 0;

QY 1 LKTAAPNCTGFGTGNNSATVYVQLSRDIALGVQVDSHVAWGKLDNDADP 60
DB 23 LKTAAPNCTGFGTGNNSATVYVQLSRDIALGVQVDSHVAWGKLDNDADP 72
QY 61 DTHVWVSEPLRSTKRYLFFVPPQVSVSDTYDICEGNDTNEPAVRFSS 120
DB 83 DTHVWVSEPLRSTKRYLFFVPPQVSVSDTYDICEGNDTNEPAVRFSS 132
QY 121 RFTVEPEFAVPLHAPQVAIVDAIYVILVQKLEKLVNWDGKNSVFRSQ 180
DB 143 RFTVEPEFAVPLHAPQVAIVDAIYVILVQKLEKLVNWDGKNSVFRSQ 192
QY 181 WSKIRLWTSFTQWLPFGSDUTTPFCHADRIWAGKLGAGVPGALPPNQANG 240
DB 203 WSKIRLWTSFTQWLPFGSDUTTPFCHADRIWAGKLGAGVPGALPPNQANG 262
QY 241 LSPDLQAALSDNYPTVWML 259
DB 263 LSPDLQAALSDNYPTVWML 281

RESULT 5 PRELIMINARY; PRT; 272 AA.
ID Q9GL63
AC Q9GL63; Q9GL62;
DT 01-DEC-2002 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Epithelial lens deoxyribonuclease I (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivordia; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1] Taxid=9913;
RP SEQUENCE FROM N.A.
RA De Maria A.B.; Sanguinetti C.J.; Arruti C.;
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF311922; AAG28792.2; -.
DR InterPro; IPR001582; DNase_I.
DR PRINTS; PF03370; Exo_endo_Phos.
DR PROSITE; PS00919; DNase_I_1.
DR PROSITE; PS00918; DNase_I_2.
DR SMART; SM001582; DNaseI_1.
DR PROSITE; PS00919; DNase_I_1.
DR PROSITE; PS00918; DNase_I_2.
SQ SEQUENCE 272 AA; 30179 MW; D808689AD4846 CRC64;

Query Match 58.8%; Score 804; DB 13; Length 282;
Best Local Similarity 58.8%; Pred. No. 84e-71;
Matches 152; Conservative 43; Mismatches 65; Indels 0; Gaps 0;

QY 1 LKTAAPNCTGFGTGNNSATVYVQLSRDIALGVQVDSHVAWGKLDNDADP 60
DB 21 LKTAAPNCTGFGTGNNSATVYVQLSRDIALGVQVDSHVAWGKLDNDADP 80
QY 61 DTHVWVSEPLRSTKRYLFFVPPQVSVSDTYDICEGNDTNEPAVRFSS 120

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QY 121 RFTVEFALVPLAARPDVAIADYDVLQVKEGLDVLGMDGNAGSVRFQ 180
 140 UTTELACPAVGLRTPVAVRQVGLQWEDNAGLQGLDVLGMDGNAGSVRFQ 199
 QY 181 MSSIKLWTSPTQMLPISADTT-ATPHCKYDVIYVAGLGVAVQSDALFHFQAY 239
 DB 200 WPHLQGLQSSGLQGLDVLGMDGNAGSVRFQVAVRQVGLQWEDNAGLQGLDVLGMDGNAGSVRFQ 259
 QY 240 GLSDQLAQALSDHPTFVWMLK 260
 DB 260 LUTTEKAAVSDHPTFVWMLK 260

RESULT 14
 ID 097068 PRELIMINARY; PRT: 350 AA.
 AC Q97068 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Deoxyribonuclease I.
 GN DNASEI.
 GN Eukaryotic Metazoan Chordata, Craniata; Vertebrata; Murelesomati;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 RN [1]-TaxID=8355;
 RP SEQUENCE FROM N.A.
 RC TISSUE=pancreas;
 RA Shokawa D., Tanuma S.; DNase gamma, P.
 RA Submitted (D96-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF059612; AAC64266.1; -.
 DR HSSP; P00639; 3DM12; DNase I.
 DR InterPro; IPR005135; Exo endo phos.
 DR Pfam; PF03372; Exo endo phos; 1.
 DR PRINTS; PR00130; DNASEI.
 DR ProDom; PD005408; DNASEI.
 DR SMART; SM00476; DNaseI; 1.
 DR PROSITE; PS00919; DNASEI 1; 1.
 SQ SEQUENCE 350 AA; 39265 MW; 7CB66AFC91BCE70 CRC64;
 Query Match 46.0%; Score 626.5; DB 13; Length 350;
 Matches 116; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 21 KIAANNITQFTGNSMNAIVSYVQLLSRYHIALVQEVDSHLVANGKLDNLN-AD 61
 DB 21 KIAANNITQFTGNSMNAIVSYVQLLSRYHIALVQEVDSHLVANGKLDNLN-AD 61
 QY 62 FYHVSPELQSKYETLVYTPDPDQVSDSYVDGCEPQSDYTPNEPVALFFSR 121
 DB 81 NYNLISBGLSSSTENAVYVDELVWPTVHTFDGNGDTSFIREPVAFTSL 140
 QY 122 FTEVEPVALVPLAARPDVAIADYDVLQVKEGLDVLGMDGNAGSVRFQ 181
 DB 141 LUTTEKAAVSDHPTFVWMLK 260
 QY 182 SSRIKLSPTQMLPISADTT-ATPHCKYDVIYVAGLGVAVQSDALFHFQAY 239
 DB 201 LUTTEKAAVSDHPTFVWMLK 260
 QY 241 GLSDQLAQALSDHPTFVWMLK 260
 DB 261 LUTTEKAAVSDHPTFVWMLK 260

RESULT 15
 ID 097104 PRELIMINARY; PRT: 295 AA.
 AC Q97104 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Deoxyribonuclease gamma.
 GN Xenopus laevis (African clawed frog).
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 RN [1]-TaxID=8355;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Shokawa D., Tanuma S.; DNase gamma, P.
 RA Submitted (D96-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF059612; AAC64266.1; -.
 DR HSSP; P00639; 2DM12; DNase I.
 DR InterPro; IPR005135; Exo endo phos.
 DR Pfam; PF03372; Exo endo phos; 1.
 DR PRINTS; PR00130; DNASEI.
 DR ProDom; PD005408; DNASEI.
 DR SMART; SM00476; DNaseI; 1.
 DR PROSITE; PS00919; DNASEI 1; 1.
 SQ SEQUENCE 295 AA; 34223 MW; BHS5CTFCFFIAC80 CRC64;
 Query Match 45.9%; Score 628; DB 13; Length 295;
 Best Local Similarity 47.9%; Pred. No. 28-53;
 Matches 136; Conservative 47; Mismatches 86; Indels 4; Gaps 3;
 QY 1 LKTAANITQFTGNSMNAIVSYVQLLSRYHIALVQEVDSHLVANGKLDNLN-CD 58
 DB 18 LRICSPVQSGSKDKEPAVWVVKRLISKCDITLMEKDSNTVIRLLMAQNGSE 77
 QY 59 ADPTVYVVSPELQSKYETLVYTPDPDQVSDSYVDGCEPQSDYTPNEPVALVF 118
 DB 78 TNQFDUTLSQRLGKSTKSGQGYIKRLVSYVQVTKD-LQDSDAFSREPVVWF 136
 QY 119 FSRFTVEPVALVPLAARPDVAIADYDVLQVKEGLDVLGMDGNAGSVRFQ 178
 DB 137 QNSSTKLSPTQMLPISADTT-ATPHCKYDVIYVAGLGVAVQSDALFHFQ 217
 QY 179 SQSSIKLSPTQMLPISADTT-ATPHCKYDVIYVAGLGVAVQSDALFHFQ 237
 DB 197 LKTAANITQFTGNSMNAIVSYVQLLSRYHIALVQEVDSHLVANGKLDNLN-CD 58
 QY 238 AVGLSDQLAQALSDHPTFVWMLK 260
 DB 257 AVGLTEQSLQVSDHPTFVWMLK 279

Search completed: November 21, 2003, 13:56:34
 Job time : 42 secs

GenCore version 5.1.6
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ON protein - protein search, using sw model

Run on: November 21, 2003, 13:46:51 ; Search time 21 Seconds
(without alignments)
523.449 Million call updates/sec

Title: us-10-005-306-9

Perfect score: 1367

Sequence: 1 LKIAAFNIQFQTSRGNAT.....LSQIAQAISHHIVEMLK 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searches: 328717 seqs, 42310058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database: 1 Issued Patents AA*
2 /cgn2_6/prodata/1/aa/5b COMB pep*
3 /cgn2_6/prodata/1/aa/5b COMB pep*
4 /cgn2_6/prodata/1/aa/5b COMB pep*
5 /cgn2_6/prodata/1/aa/5b COMB pep*
6 /cgn2_6/prodata/1/aa/backfiles pep*

Pred. No. is the number of results predicted by chance to have a
score at least as high as the observed score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|------------------|-------------------|
| 2 | 1367 | 100.0 | 260 | US-08-663-831-0 | Sequence 9, Appl |
| 3 | 1362 | 99.6 | 260 | US-09-786-774-1 | Sequence 1, Appl |
| 4 | 1362 | 99.6 | 260 | US-08-663-831-1 | Sequence 1, Appl |
| 5 | 1362 | 99.6 | 260 | US-09-786-774-1 | Sequence 1, Appl |
| 6 | 1362 | 99.6 | 260 | US-09-786-774-1 | Sequence 1, Appl |
| 7 | 1362 | 99.6 | 348 | US-07-895-300A-1 | Sequence 1, Appl |
| 8 | 1362 | 99.6 | 348 | US-09-638-112-1 | Sequence 1, Appl |
| 9 | 1362 | 99.6 | 260 | US-08-663-831-1 | Sequence 1, Appl |
| 10 | 1362 | 99.6 | 260 | US-08-663-831-1 | Sequence 1, Appl |
| 11 | 1358 | 99.3 | 260 | US-08-663-831-3 | Sequence 3, Appl |
| 12 | 1358 | 99.3 | 260 | US-08-663-831-11 | Sequence 11, Appl |
| 13 | 1358 | 99.3 | 260 | US-08-663-831-15 | Sequence 15, Appl |
| 14 | 1357 | 99.3 | 260 | US-08-663-831-1 | Sequence 1, Appl |
| 15 | 1357 | 99.3 | 348 | US-08-663-831-1 | Sequence 1, Appl |
| 16 | 1356 | 99.2 | 260 | US-08-663-831-5 | Sequence 5, Appl |
| 17 | 1356 | 99.2 | 260 | US-08-663-831-6 | Sequence 6, Appl |
| 18 | 1356 | 99.2 | 260 | US-08-663-831-13 | Sequence 13, Appl |
| 19 | 1356 | 99.2 | 260 | US-08-663-831-13 | Sequence 13, Appl |
| 20 | 1356 | 99.2 | 260 | US-08-663-831-16 | Sequence 16, Appl |
| 21 | 1354 | 99.0 | 260 | US-08-663-831-8 | Sequence 8, Appl |
| 22 | 1354 | 99.0 | 260 | US-08-663-831-8 | Sequence 8, Appl |
| 23 | 1352 | 98.9 | 260 | US-08-663-831-17 | Sequence 17, Appl |
| 24 | 592 | 43.3 | 310 | US-08-640-765A-1 | Sequence 1, Appl |
| 25 | 592 | 43.3 | 310 | US-09-073-613-1 | Sequence 1, Appl |
| 26 | 591 | 43.2 | 385 | US-10-074-509-2 | Sequence 2, Appl |
| 27 | 591 | 43.2 | 303 | US-10-074-509-2 | Sequence 2, Appl |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 463.5 | 33.9 | 302 | 4 | US-08-662-745A-2 | Sequence 2, Appl |
| 29 | 463.5 | 33.9 | 302 | 4 | US-08-662-745A-2 | Sequence 2, Appl |
| 30 | 461.6 | 33.8 | 351 | 3 | US-09-084-989-2 | Sequence 2, Appl |
| 31 | 454 | 33.2 | 113 | 3 | US-08-406-030A-29 | Sequence 29, Appl |
| 32 | 193 | 14.1 | 38 | 1 | US-07-895-300A-17 | Sequence 17, Appl |
| 33 | 193 | 14.1 | 38 | 1 | US-07-895-300A-17 | Sequence 17, Appl |
| 34 | 193 | 14.1 | 38 | 4 | US-09-638-112-17 | Sequence 17, Appl |
| 35 | 193 | 14.1 | 38 | 4 | US-09-638-112-17 | Sequence 17, Appl |
| 36 | 186 | 13.6 | 32 | 1 | US-07-895-300A-9 | Sequence 9, Appl |
| 37 | 186 | 13.6 | 32 | 1 | US-07-895-300A-9 | Sequence 9, Appl |
| 38 | 186 | 13.6 | 32 | 1 | US-09-638-112-9 | Sequence 9, Appl |
| 39 | 186 | 13.6 | 32 | 5 | US-09-638-112-9 | Sequence 9, Appl |
| 40 | 163 | 11.9 | 28 | 1 | US-07-895-300A-15 | Sequence 15, Appl |
| 41 | 163 | 11.9 | 28 | 1 | US-07-895-300A-15 | Sequence 15, Appl |
| 42 | 163 | 11.9 | 28 | 1 | US-08-458-367-15 | Sequence 15, Appl |
| 43 | 163 | 11.9 | 28 | 5 | US-08-458-367-15 | Sequence 15, Appl |
| 44 | 157 | 11.5 | 28 | 1 | US-07-895-300A-14 | Sequence 14, Appl |
| 45 | 157 | 11.5 | 28 | 1 | US-08-458-367-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-08-663-831-9
Sequence 9, Application US/08663811
US-08-663-831-9
GENERAL INFORMATION:
APPLICANT: Lazarus, Robert A.
APPLICANT: Pan Clark Oun
INVENTOR: PAN CLARK OUN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
ADDRESS: 460 Point San Francisco Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION: 442
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,831
FILING DATE: 14-Jun-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnathon, Sean A.
REGISTRATION NUMBER: 35,910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/922-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TOPOLOGY: Linear

Query Match 100.00; Score 1367; DB 4; Length 260;
Basic Local Similarity 100.00; P-Val: 6e-51;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKIAAFNIQFQTSRGNATVSYVLSHIVLIVETVRSHLPAQGLLINDQAP 60
DB 1 LKIAAFNIQFQTSRGNATVSYVLSHIVLIVETVRSHLPAQGLLINDQAP 60
QY 61 DTHWVSPFGKSTKTEFLTVPVQSVASVSTVDDCEFGQNTFRAPALVRFPS 120

Db 61 DTHVYVSEPLGRSKYKRYLVPRPOVSANDSVYDDGCFPCGNDTNRFPALVRFSS 120
 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180
 Db 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180
 Qy 181 MSIRLWSTPFOMLIPDSADTATPHCATYDRIWAGLLAGAVPDSALPFPNQAYG 240
 Db 181 MSIRLWSTPFOMLIPDSADTATPHCATYDRIWAGLLAGAVPDSALPFPNQAYG 240
 Qy 241 LSOLAQAISDHYVFWMLK 260
 Db 241 LSOLAQAISDHYVFWMLK 260

RESULT 2

US-08-663-831-10
 ; Sequence 10, Application US/08663831

; Patent No. 6391609.

; GENERAL INFORMATION:

; APPLICANT: Lazarus, Robert A.

; APPLICANT: Pan, Clark Qun

; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER: IBM PC compatible

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; SOFTWARE: GENENTECH

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Minipain (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/663,831

; FILING DATE: 28-Feb-2001

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Johnston, Sean A.

; REGISTRATION NUMBER: 35,910

; REFERENCE/DOCKET NUMBER: P0925P1C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-3562

; TELEFAX: 910/371-7189

; TELEPHONE: 650/225-3562

; TELEFAX: 650/952-9081

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; TYPE: 260 amino acids

; LENGTH: 260

; TOPOLOGY: Linear

; US-08-663-831-10

Query Match 99.61; Score 1364; DB 4; Length 260;

Best Local Similarity 99.61; Pred. No. 8e-151;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTAAPLQIFGFTGNSNATVYVQLLSRVDLWQVDSHLVAVGKLLNDADP 60
 Db 1 LKTAAPLQIFGFTGNSNATVYVQLLSRVDLWQVDSHLVAVGKLLNDADP 60
 Qy 61 DTHVYVSEPLGRSKYKRYLVPRPOVSANDSVYDDGCFPCGNDTNRFPALVRFSS 120
 Db 61 DTHVYVSEPLGRSKYKRYLVPRPOVSANDSVYDDGCFPCGNDTNRFPALVRFSS 120
 Qy 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180
 Db 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180
 Qy 181 MSIRLWSTPFOMLIPDSADTATPHCATYDRIWAGLLAGAVPDSALPFPNQAYG 240

Db 181 MSIRLWSTPFOMLIPDSADTATPHCATYDRIWAGLLAGAVPDSALPFPNQAYG 240
 Qy 241 LSOLAQAISDHYVFWMLK 260
 Db 241 LSOLAQAISDHYVFWMLK 260
 RESULT 3
 US-09-796-774-1
 ; Sequence 11, Application US/09796774
 ; Patent No. 615497
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Shak, Steven

; TITLE OF INVENTION: HUMAN DNASE I VARIANTS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; SOFTWARE: GENENTECH

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Minipain (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/796,774

; FILING DATE: 28-Feb-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/939995

; FILING DATE: 15-SEP-1997

; APPLICATION NUMBER: 08/540527

; FILING DATE: 24-MAR-1995

; APPLICATION NUMBER: 08/403873

; FILING DATE: 24-MAR-1995

; APPLICATION NUMBER: PCT/US95/02366

; FILING DATE: 24-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Johnston, Sean A.

; REGISTRATION NUMBER: 35,910

; REFERENCE/DOCKET NUMBER: P0925P1C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-3562

; TELEFAX: 650/952-9081

; INFORMATION FOR SEQ ID NO:13:

; SEQUENCE CHARACTERISTICS:

; TYPE: 260 amino acids

; LENGTH: 260

; TOPOLOGY: Linear

; US-09-796-774-1

Query Match 99.61; Score 1362; DB 4; Length 260;

Best Local Similarity 99.61; Pred. No. 8e-151;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTAAPLQIFGFTGNSNATVYVQLLSRVDLWQVDSHLVAVGKLLNDADP 60
 Db 1 LKTAAPLQIFGFTGNSNATVYVQLLSRVDLWQVDSHLVAVGKLLNDADP 60
 Qy 61 DTHVYVSEPLGRSKYKRYLVPRPOVSANDSVYDDGCFPCGNDTNRFPALVRFSS 120
 Db 61 DTHVYVSEPLGRSKYKRYLVPRPOVSANDSVYDDGCFPCGNDTNRFPALVRFSS 120
 Qy 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180
 Db 121 RFTVREFAVPLAARADVAEIDALYDVLQVQKGLDVLMDKDNAGCSVRFSSQ 180

QY 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240
 DB 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240
 QY 241 LSOOLAQALSHYVPEVWLK 260
 DB 241 LSOOLAQALSHYVPEVWLK 260

RESULT 4

US-08-663-831-1

; Sequence 1, Application US/08663831

; Patent No. 639607

; GENERAL INFORMATION:

; APPLICANT: Lazarus, Robert A.

; APPLICANT: Ben, Clark Qun

; TITLE OF INVENTION: HUMAN DWASE I HYPERACTIVE VARIANTS

; CORRESPONDENCE ADDRESS:

; STREET: 460 Point San Bruno Blvd

; CITY: San Bruno, California

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMMUNICATIONS FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/663,831

; FILING DATE: 14-Jun-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Jonneton, Sean A.

; REGISTRATION NUMBER: 35,910

; TELEPHONE: 415/225-3562

; TELEFAX: 415/952-9881

; TELECOMMUNICATION INFORMATION:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 260 amino acids

; TOPOLOGY: Linear

US-08-663-831-1

Query Match 99.6%; Score 1362; DB 4; Length 260;

Best Local Similarity 99.6%; Pred. No. 1.4e-150; Indels 0; Gaps 0;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAATPTQGTGTSNATVSVYVQLLSYDALVQVSRHSLTAVGCLLQADAP 60

DB 1 LKTAATPTQGTGTSNATVSVYVQLLSYDALVQVSRHSLTAVGCLLQADAP 60

QY 61 DTVHVVSEPLRGSTKSVFLPYRPOQVSNVSYVTDGCEFCQNTFNREPAIVRFS 120

DB 61 DTVHVVSEPLRGSTKSVFLPYRPOQVSNVSYVTDGCEFCQNTFNREPAIVRFS 120

QY 121 EPTVEFEALVPLHAPQDAVETALDYVTLVQVKGLELQVADGNAGGCVSFPSQ 180

DB 121 EPTVEFEALVPLHAPQDAVETALDYVTLVQVKGLELQVADGNAGGCVSFPSQ 180

QY 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240

DB 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240

QY 241 LSOOLAQALSHYVPEVWLK 260

DB 241 LSOOLAQALSHYVPEVWLK 260

RESULT 5

US-08-663-831-14

; Sequence 14, Application US/08663831

; Patent No. 639607

; GENERAL INFORMATION:

; APPLICANT: Lazarus, Robert A.

; APPLICANT: Ben, Clark Qun

; TITLE OF INVENTION: HUMAN DWASE I HYPERACTIVE VARIANTS

; CORRESPONDENCE ADDRESS:

; STREET: 460 Point San Bruno Blvd

; CITY: San Bruno, California

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMMUNICATIONS FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/663,831

; FILING DATE: 14-Jun-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Jonneton, Sean A.

; REGISTRATION NUMBER: 35,910

; TELEPHONE: 415/225-3562

; TELEFAX: 415/952-9881

; TELECOMMUNICATION INFORMATION:

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 260 amino acids

; TOPOLOGY: Linear

US-08-663-831-14

Query Match 99.6%; Score 1362; DB 4; Length 260;

Best Local Similarity 99.6%; Pred. No. 1.4e-150; Indels 0; Gaps 0;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAATPTQGTGTSNATVSVYVQLLSYDALVQVSRHSLTAVGCLLQADAP 60

DB 1 LKTAATPTQGTGTSNATVSVYVQLLSYDALVQVSRHSLTAVGCLLQADAP 60

QY 61 DTVHVVSEPLRGSTKSVFLPYRPOQVSNVSYVTDGCEFCQNTFNREPAIVRFS 120

DB 61 DTVHVVSEPLRGSTKSVFLPYRPOQVSNVSYVTDGCEFCQNTFNREPAIVRFS 120

QY 121 EPTVEFEALVPLHAPQDAVETALDYVTLVQVKGLELQVADGNAGGCVSFPSQ 180

DB 121 EPTVEFEALVPLHAPQDAVETALDYVTLVQVKGLELQVADGNAGGCVSFPSQ 180

QY 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240

DB 181 WSSILATSTPTQMLPPSADTATTTTCNATVWALAGAVVPSALPNNQANG 240

QY 241 LSOOLAQALSHYVPEVWLK 260

DB 241 LSOOLAQALSHYVPEVWLK 260

RESULT 6

US-10-074-509-4

; Sequence 4, Application US/10074509

; Patent No. 639607

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.


```

/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ 1.44 Mb floppy disk
/
/ TITLE OF INVENTION: PC-DOS/MS-DOS
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Minipatin (Genentech)
/ CURRENT APPLICATION NUMBER: US/09/638-112
/ FILING DATE: 09-Aug-2000
/
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ REGISTRATION NUMBER: 08/942561
/ FILING DATE: 01-OCT-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Johnston, Sean A.
/ REGISTRATION NUMBER: 910
/ REFERENCE/DOCKET NUMBER: P0747C7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-3562
/ TELEFAX: 650/225-3561
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 346 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ US-09-638-112-1

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Query Match Similarity 99.6%; Score 1362; DB 4; Length 346;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LKTAAPNQTGGTNSNATLVSVIOLLRSYDIALVOEVRDSHTVANGKLLNQADP 60
DB 76 LKTAAPNQTGGTNSNATLVSVIOLLRSYDIALVOEVRDSHTVANGKLLNQADP 135
QY 61 DTHVYVSPFGKSTKRYLVVRPDQVANSYVDGCEPCQNDTFNRPALVRFSS 120
DB 136 DTHVYVSPFGKSTKRYLVVRPDQVANSYVDGCEPCQNDTFNRPALVRFSS 195
QY 121 RTFVREFPAIVFHAAPGDAEADALDYVLDOEKGLEDVMDGDFNAGCSYVRSO 180
DB 196 RTFVREFPAIVFHAAPGDAEADALDYVLDOEKGLEDVMDGDFNAGCSYVRSO 255
QY 181 MSSRLMTSTFQMLIPDSATTTATPHCAVDRIVVGMLRGAVPDSALPFFOAYG 240
DB 256 MSSRLMTSTFQMLIPDSATTTATPHCAVDRIVVGMLRGAVPDSALPFFOAYG 315
QY 241 LSQQLAQLSDHPVFWMLK 260
DB 316 LSQQLAQLSDHPVFWMLK 335

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RESULT 9

PCT-US93-05136-1

Sequence 2; Application PC/TU990305136

Parent No. 6391607

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: PURIFIED FORMS OF Dnaase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

5.25 inch, 360 Kb floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Minipatin (Genentech)
/ CURRENT APPLICATION DATA: US/93/05136
/ FILING DATE: 19930528
/
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ REGISTRATION NUMBER:
/ FILING DATE:
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Johnston, Sean A.
/ REGISTRATION NUMBER: P35, 910
/ REFERENCE/DOCKET NUMBER: PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-3562
/ TELEFAX: 415/952-9881
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 346 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: Linear
/
/ PCT-US93-05136-1

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Query Match Similarity 99.6%; Score 1362; DB 5; Length 346;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LKTAAPNQTGGTNSNATLVSVIOLLRSYDIALVOEVRDSHTVANGKLLNQADP 60
DB 76 LKTAAPNQTGGTNSNATLVSVIOLLRSYDIALVOEVRDSHTVANGKLLNQADP 135
QY 61 DTHVYVSPFGKSTKRYLVVRPDQVANSYVDGCEPCQNDTFNRPALVRFSS 120
DB 136 DTHVYVSPFGKSTKRYLVVRPDQVANSYVDGCEPCQNDTFNRPALVRFSS 195
QY 121 RTFVREFPAIVFHAAPGDAEADALDYVLDOEKGLEDVMDGDFNAGCSYVRSO 180
DB 196 RTFVREFPAIVFHAAPGDAEADALDYVLDOEKGLEDVMDGDFNAGCSYVRSO 255
QY 181 MSSRLMTSTFQMLIPDSATTTATPHCAVDRIVVGMLRGAVPDSALPFFOAYG 240
DB 256 MSSRLMTSTFQMLIPDSATTTATPHCAVDRIVVGMLRGAVPDSALPFFOAYG 315
QY 241 LSQQLAQLSDHPVFWMLK 260
DB 316 LSQQLAQLSDHPVFWMLK 335

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RESULT 10

US-08-663-831-2

Sequence 2; Application US/08663831

Parent No. 6391607

GENERAL INFORMATION:

APPLICANT: Lazarus, Robert A.

APPLICANT: Pat. Clark Gun

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Minipatin (Genentech)

CURRENT APPLICATION:

APPLICATION NUMBER: US/08/663,831

Mon Nov 24 10:03:07 2003

// FILING DATE: 14-Jun-1996
 // TELETYPE: 910/371-7168
 // ATTORNEY/AGENT INFORMATION:
 // NAME: Johnston, Sean A.
 // REGISTRATION NUMBER: 35,910
 // REFERENCE/DOCKET NUMBER: P1042
 // TELEPHONE: 415/225-3562
 // TELEFAX: 415/952-9881
 // TELETYPE: 910/371-7168
 // INFORMATION: 2:
 // SEQUENCE CHARACTERISTICS:
 // LENGTH: 260 amino acids
 // TYPE: Amino Acid
 // TOPOLOGY: Linear
 // US-08-663-831-2

Query March 99.3%; Score 1358; DB 4; Length 260;
 Best Local Similarity 99.3%; Pred. No. 4e-150;
 Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKTAENKQFTGEGMSNATVSVQLSRVDALVQEVDSHLTAVGKLLNDAP 60
 DB 1 LKTAENKQFTGEGMSNATVSVQLSRVDALVQEVDSHLTAVGKLLNDAP 60
 QY 61 DTHVWSEPLGRKSTKRYLFVTPPOVSAVSYVDGCEPCGNDTFRPALVFFS 120
 QY 61 DTHVWSEPLGRKSTKRYLFVTPPOVSAVSYVDGCEPCGNDTFRPALVFFS 120
 DB 61 DTHVWSEPLGRKSTKRYLFVTPPOVSAVSYVDGCEPCGNDTFRPALVFFS 120
 QY 121 RFTVEFPAVLVLAHAPDVAEIDALYDVLQVKEGLEDVLMGDFNAGCSVFP 180
 DB 121 RFTVEFPAVLVLAHAPDVAEIDALYDVLQVKEGLEDVLMGDFNAGCSVFP 180
 QY 181 WSSILRTSPTFQMLPDSADTTPHCAVDIVAGLLECAVWPDSALFFNFOA 240
 DB 181 WSSILRTSPTFQMLPDSADTTPHCAVDIVAGLLECAVWPDSALFFNFOA 240
 QY 241 LSDLQAQLSDHYFVEMWLK 260
 DB 241 LSDLQAQLSDHYFVEMWLK 260

RESULT 11
 // Sequence 11, Application US/08663831
 // Patent No. 6391607
 // GENERAL INFORMATION:
 // APPLICANT: Lazarus, Robert A.
 // TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 // NUMBER OF SEQUENCES: 17
 // CORRESPONDENCE ADDRESS:
 // ADDRESSEE: Genentech, Inc.
 // ADDRESS: 460 Point San Bruno Blvd
 // CITY: South San Francisco
 // STATE: California
 // COUNTRY: USA
 // FILING DATE: 14-Jun-1996
 // PUBLICATION DATE: 14-Jun-1996
 // TELEFAX: 415/952-9881
 // TELETYPE: 910/371-7168
 // INFORMATION FOR SEQ ID NO: 1:
 // NAME: Johnston, Sean A.
 // REGISTRATION NUMBER: 35,910
 // REFERENCE/DOCKET NUMBER: P1042
 // TELEPHONE: 415/225-3562
 // TELEFAX: 415/952-9881
 // TOPOLOGY: Linear
 // US-08-663-831-3

// TELEFAX: 415/952-9881
 // TELETYPE: 910/371-7168
 // INFORMATION FOR SEQ ID NO: 3:
 // SEQUENCE CHARACTERISTICS:
 // LENGTH: 260 amino acids
 // TYPE: Amino Acid
 // TOPOLOGY: Linear
 // US-08-663-831-3
 Query March 99.3%; Score 1358; DB 4; Length 260;
 Best Local Similarity 99.3%; Pred. No. 4e-150;
 Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKTAENKQFTGEGMSNATVSVQLSRVDALVQEVDSHLTAVGKLLNDAP 60
 DB 1 LKTAENKQFTGEGMSNATVSVQLSRVDALVQEVDSHLTAVGKLLNDAP 60
 QY 61 DTHVWSEPLGRKSTKRYLFVTPPOVSAVSYVDGCEPCGNDTFRPALVFFS 120
 DB 61 DTHVWSEPLGRKSTKRYLFVTPPOVSAVSYVDGCEPCGNDTFRPALVFFS 120
 QY 121 RFTVEFPAVLVLAHAPDVAEIDALYDVLQVKEGLEDVLMGDFNAGCSVFP 180
 DB 121 RFTVEFPAVLVLAHAPDVAEIDALYDVLQVKEGLEDVLMGDFNAGCSVFP 180
 QY 181 WSSILRTSPTFQMLPDSADTTPHCAVDIVAGLLECAVWPDSALFFNFOA 240
 DB 181 WSSILRTSPTFQMLPDSADTTPHCAVDIVAGLLECAVWPDSALFFNFOA 240
 QY 241 LSDLQAQLSDHYFVEMWLK 260
 DB 241 LSDLQAQLSDHYFVEMWLK 260
 RESULT 12
 // Sequence 11, Application US/08663831
 // Patent No. 6391607
 // GENERAL INFORMATION:
 // APPLICANT: Lazarus, Robert A.
 // TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 // NUMBER OF SEQUENCES: 17
 // CORRESPONDENCE ADDRESS:
 // ADDRESSEE: Genentech, Inc.
 // ADDRESS: 460 Point San Bruno Blvd
 // CITY: South San Francisco
 // STATE: California
 // COUNTRY: USA
 // FILING DATE: 14-Jun-1996
 // PUBLICATION DATE: 14-Jun-1996
 // TELEFAX: 415/952-9881
 // TELETYPE: 910/371-7168
 // INFORMATION FOR SEQ ID NO: 11:
 // NAME: Johnston, Sean A.
 // REGISTRATION NUMBER: 35,910
 // REFERENCE/DOCKET NUMBER: P1042
 // TELEPHONE: 415/225-3562
 // TELEFAX: 415/952-9881
 // TOPOLOGY: Linear
 // US-08-663-831-11

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Query Match          99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60
DB 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60

QY 61 DTHVYVSEPLGRSKYKERVLPVPODVSADVSTYDDCCPCGNDTFNREPAIVRFS 120
DB 61 DTHVYVSEPLGRSKYKERVLPVPODVSADVSTYDDCCPCGNDTFNREPAIVRFS 120

QY 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180
DB 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180

QY 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180
DB 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180

QY 181 WSSIRLSTPFTQWLIPSDATATPHCAVDRIVVAAGLKGAVVPDSALPFPQAAYG 240
DB 181 WSSIRLSTPFTQWLIPSDATATPHCAVDRIVVAAGLKGAVVPDSALPFPQAAYG 240

QY 181 WSSIRLSTPFTQWLIPSDATATPHCAVDRIVVAAGLKGAVVPDSALPFPQAAYG 240
DB 181 WSSIRLSTPFTQWLIPSDATATPHCAVDRIVVAAGLKGAVVPDSALPFPQAAYG 240

QY 241 LSOLAQAQISDHYVPEWMLK 260
DB 241 LSOLAQAQISDHYVPEWMLK 260

RESULT 14
US-08-663-831-4
; Sequence 15, Application US/08663811
; Patent No. 4e-150;
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: MIPATIN (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; NAME: Johnsen, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-663-831-4

Query Match          99.3%; Score 1357; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 5.2e-150;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60
DB 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60

QY 61 DTHVYVSEPLGRSKYKERVLPVPODVSADVSTYDDCCPCGNDTFNREPAIVRFS 120
DB 61 DTHVYVSEPLGRSKYKERVLPVPODVSADVSTYDDCCPCGNDTFNREPAIVRFS 120

QY 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180
DB 121 RFEVREFAIVPLHAPAGDAVAEDALDYDVLVQVWGLDVLMDGDFNAGCSYVRPQ 180

RESULT 15
US-08-663-831-15
; Sequence 15, Application US/08663811
; Patent No. 4e-150;
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: MIPATIN (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; NAME: Johnsen, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-663-831-15

Query Match          99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60
DB 1 LKTAAFNITGFTGTSNATVSVIQLSRDIALVQVDSHSHVAVGKLLNDADAP 60

```

QY 181 WSSIRLMTSPFOHLPDSATTTATPHCNVDRIVAGMLLRGVVPSALPFPQAAVG 240
 Db 181 WSSIRLMTSPFOHLPDSATTTATPHCNVDRIVAGMLLRGVVPSALPFPQAAVG 240
 QY 241 LSDOLAQISDRHPVEVWLK 260
 Db 241 LSDOLAQISDRHPVEVWLK 260

RESULT 15

US-08-458-367-1
 ; Sequence 1, Application US/08458367
 ; Patent No. 5783433
 ; GENINVENTOR: JOHN
 ; APPLICANT: Presz, John
 ; APPLICANT: Shice, Steven J.
 ; APPLICANT: Silkowski, Mary B.
 ; APPLICANT: TINKER, JAMES C.
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: 460 Genentech, Inc.
 ; ADDRESS: 460 Genentech, Inc.
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94060
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: GENESYS
 ; SOFTWARE: MIPatlin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/458,367
 ; FILING DATE: 02-SEP-1993
 ; CLASSIFICATION: 415
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/409631
 ; FILING DATE: 02-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346284
 ; FILING DATE: 30-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/116186
 ; FILING DATE: 02-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/695300
 ; FILING DATE: 08-JUN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnston, Sean A.
 ; ADDRESS: 910
 ; TELEPHONE: 415/225-3562
 ; TELEFAX: 415/742-1681
 ; REFERENCE/DOCENT INFORMATION:
 ; REFERENCE/DOCENT NUMBER: 20747C4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3562
 ; TELEFAX: 415/742-1681
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear

US-08-458-367-1

Query Match 98.3%; Score 1357; DB 1; Length 346;
 Best Local Similarity 99.2%; Pred. No. 8, 1e-150;
 Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKATAPFOTGTHNSATLSTVTLGSHYFALVQWRSKLVNGLNANVQAP 60
 Db 76 LKATAPFOTGTHNSATLSTVTLGSHYFALVQWRSKLVNGLNANVQAP 135
 QY 61 LKATAPFOTGTHNSATLSTVTLGSHYFALVQWRSKLVNGLNANVQAP 120

Db 136 DTHYVVSBLGRNSYKERYLFYRPQGVAGDYSYYIDGCEPCGNOTNREPAIVRFS 195
 QY 121 RFTVREPAIVPLHAAQGVAVETDALYDVLVDQERKGLDNLMDGFNAGSYVRPQ 180
 Db 196 RFTVREPAIVPLHAAQGVAVETDALYDVLVDQERKGLDNLMDGFNAGSYVRPQ 255
 QY 181 WSSIRLMTSPFOHLPDSATTTATPHCNVDRIVAGMLLRGVVPSALPFPQAAVG 240
 Db 256 WSSIRLMTSPFOHLPDSATTTATPHCNVDRIVAGMLLRGVVPSALPFPQAAVG 315
 QY 241 LSDOLAQISDRHPVEVWLK 260
 Db 316 LSDOLAQISDRHPVEVWLK 335

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GenCore version 5.1.6
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COM protein - protein search, using sw model

Run on: November 21, 2003, 13:56:42 ; Search time 30 Seconds

(without alignments)
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perfect score: 136 /
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BY ORDER OF THE BOARD OF DIRECTORS:

Gapop 10.

Searched: 666188 se

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✓ quasi non con inter in

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Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Published Applications 22.4

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and is derived by analysis of the total score distribution

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| 100 | 100 |

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| 3 | 90 | 90 | 90 | 90 | 90 | 90 |
| 4 | 85 | 85 | 85 | 85 | 85 | 85 |
| 5 | 80 | 80 | 80 | 80 | 80 | 80 |
| 6 | 75 | 75 | 75 | 75 | 75 | 75 |
| 7 | 70 | 70 | 70 | 70 | 70 | 70 |
| 8 | 65 | 65 | 65 | 65 | 65 | 65 |
| 9 | 60 | 60 | 60 | 60 | 60 | 60 |
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| 18 | 15 | 15 | 15 | 15 | 15 | 15 |
| 19 | 10 | 10 | 10 | 10 | 10 | 10 |
| 20 | 5 | 5 | 5 | 5 | 5 | 5 |

| Sequence 9, | Sequence 10 |
|-------------------------------------|-------------------------------------|
| 1 1367 100.0 260 14 US-10-005-306-9 | 2 1364 99.8 260 14 US-10-005-306-10 |

| Sequence 3, | US-09-825-012-3 |
|-------------|-----------------|
| 3 | 1362 |
| 3 | 99.6 |
| 3 | 260 |
| 3 | 10 |

SUMMARIES

| Result No. | Score | Query | Match | Length | ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 1367 | 100-0 | 260 | 14 | US-1-005-3062-9 | Sequence 10, April |
| 2 | 1367 | 100-0 | 260 | 14 | US-1-005-3062-9 | Sequence 10, April |
| 3 | 1362 | 99-6 | 260 | 10 | US-08-895-023-0 | Sequence 4, April |
| 4 | 1362 | 99-6 | 260 | 10 | US-08-895-023-0 | Sequence 4, April |
| 5 | 1362 | 99-6 | 260 | 14 | US-1-133-085-4 | Sequence 4, April |
| 6 | 1362 | 99-6 | 260 | 14 | US-1-133-085-4 | Sequence 4, April |
| 7 | 1362 | 99-6 | 260 | 4 | US-1-105-309-1 | Sequence 1, April |
| 8 | 1362 | 99-6 | 260 | 4 | US-1-105-309-1 | Sequence 1, April |
| 9 | 1362 | 99-6 | 260 | 4 | US-1-105-306-1 | Sequence 14, April |
| 10 | 1362 | 99-6 | 260 | 4 | US-1-105-306-1 | Sequence 14, April |
| 11 | 1362 | 99-6 | 260 | 10 | US-10-095-675-1 | Sequence 1, April |
| 12 | 1362 | 99-6 | 260 | 10 | US-10-095-675-1 | Sequence 1, April |
| 13 | 1362 | 99-6 | 282 | 15 | US-0-005-625-13 | Sequence 11, April |
| 14 | 1362 | 99-6 | 346 | 15 | US-0-155-407-1 | Sequence 1, April |
| 15 | 1362 | 99-6 | 515 | 10 | US-08-825-012-66 | Sequence 66, April |
| 16 | 1362 | 99-6 | 515 | 10 | US-08-825-012-66 | Sequence 66, April |
| 17 | 1362 | 99-6 | 517 | 10 | US-08-025-012-78 | Sequence 78, April |
| 18 | 1362 | 99-6 | 517 | 10 | US-08-025-012-78 | Sequence 78, April |
| 19 | 1362 | 99-6 | 521 | 10 | US-08-825-012-71 | Sequence 71, April |
| 20 | 1362 | 99-6 | 521 | 10 | US-08-825-012-71 | Sequence 71, April |

ALIGNMENTS

RESULT 1

```

US-10-005-306-9 Application: US10006306
US-10-005-306-9 Title: US2002017302A2
1 GENERAL INFORMATION:
2 APPLICANT: Lazarus, Robert A.
3 INVENTOR: Lazarus, Robert A.
4 TITLE OF INVENTION: HUNKIN DYNASE I HYPERBAC
5 FILE REFERENCE: PL04231
6 CURRENT APPLICATION NUMBER: US10/009,308
7 CURRENT FILING DATE: 2002-05-21
8 PRIORITY DATE: 1996-06-14
9 PRIOR FILING DATE: 1996-06-14
10 NUMBER OF SEQ ID NOS: 17
11 SEQ ID NO 9
12 LENGTH: 260
13 ORGANISM: Homo sapiens
US-10-005-306-9

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| Query Best 1 Match | |
|--------------------------|----------|
| Qy | 0.000000 |
| Db | 0.000000 |
| Qy | 0.000000 |
| Db | 0.000000 |
| Qy | 0.000000 |
| Db | 0.000000 |
| Qy | 0.000000 |

Db 181 WSRWTWSTPTQWLIPDSNATTTATPHCAIDRIVAGMLGGAVVPDSALPFPNQAYG 240
 Qy 241 LSDQALQALSHYPPVWLK 260
 Db 241 LSDQALQALSHYPPVWLK 260

RESULT 2
 US-10-005-306-10
 ; Sequence 10, Application US/10005306
 ; Best Local Similarity 99.64; Pred. No. 1.1e-144;
 ; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Pan, Clark Qun
 ; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 ; FILE REFERENCE: P1042CL
 ; CURRENT APPLICATION NUMBER: US/10/005_306
 ; CURRENT FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: US 09/663,831
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 11
 ; SEQ ID NO 10
 ; LENGTH: 260
 ; TYPE: Amino Acid
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-10-005-306-10

Query Match 99.64; Score 1364; DB 14; Length 260;
 Best Local Similarity 99.64; Pred. No. 1.1e-144;
 Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKIAFNITCGFTGNSNATVSYVQLSRDIALVQVDSHSLTAVGKLLNNDAP 60
 Db 1 LKIAFNITCGFTGNSNATVSYVQLSRDIALVQVDSHSLTAVGKLLNNDAP 60

Qy 61 DTHVWSEPLGRSKSEYLFVYPPDQVSAVDSYVDDGCEPCGNDTFRPEALVFFS 120
 Qy 61 DTHVWSEPLGRSKSEYLFVYPPDQVSAVDSYVDDGCEPCGNDTFRPEALVFFS 120

Qy 61 DTHVWSEPLGRSKSEYLFVYPPDQVSAVDSYVDDGCEPCGNDTFRPEALVFFS 120
 Db 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180
 Qy 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180

Qy 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180
 Db 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180

Qy 181 WSRWTWSTPTQWLIPDSNATTTATPHCAIDRIVAGMLGGAVVPDSALPFPNQAYG 240
 Db 181 WSRWTWSTPTQWLIPDSNATTTATPHCAIDRIVAGMLGGAVVPDSALPFPNQAYG 240

Qy 241 LSDQALQALSHYPPVWLK 260
 Db 241 LSDQALQALSHYPPVWLK 260

RESULT 3
 US-09-825-012-3
 ; Sequence 3, Application US/09825012
 ; Patent No. US20020127798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazarus, Robert
 ; APPLICANT: Pan, Clark Qun
 ; TITLE OF INVENTION: Compounds for Targeting
 ; FILE REFERENCE: 43191-254808
 ; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US 07/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO 3
 ; LENGTH: 260
 ; TYPE: Amino Acid
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-825-012-3

Query Match 99.64; Score 1362; DB 10; Length 260;
 Best Local Similarity 99.64; Pred. No. 1.8e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAFNITCGFTGNSNATVSYVQLSRDIALVQVDSHSLTAVGKLLNNDAP 60
 Db 1 LKIAFNITCGFTGNSNATVSYVQLSRDIALVQVDSHSLTAVGKLLNNDAP 60

Qy 61 DTHVWSEPLGRSKSEYLFVYPPDQVSAVDSYVDDGCEPCGNDTFRPEALVFFS 120
 Db 61 DTHVWSEPLGRSKSEYLFVYPPDQVSAVDSYVDDGCEPCGNDTFRPEALVFFS 120

Qy 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180
 Db 121 RFTVEFAVFLHAAFGDAVATDLYDLVQVKGLEDVLMAGDFNAGGCVYPPSQ 180

Qy 181 WSRWTWSTPTQWLIPDSNATTTATPHCAIDRIVAGMLGGAVVPDSALPFPNQAYG 240
 Db 181 WSRWTWSTPTQWLIPDSNATTTATPHCAIDRIVAGMLGGAVVPDSALPFPNQAYG 240

Qy 241 LSDQALQALSHYPPVWLK 260
 Db 241 LSDQALQALSHYPPVWLK 260

RESULT 4
 US-10-133-065-4
 ; Sequence 4, Application US/10133065
 ; Publication No. US2002012322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baron, Kevin P.
 ; APPLICANT: Baron, Will F.
 ; TITLE OF INVENTION: HUMAN DNASE
 ; NUMBER OF SEQUENCES: 1
 ; CURRENT APPLICATION NUMBER: US 10/133,065
 ; ADDRESS: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; DISK: 3.5 inch, 1-44 Mb floppy disk
 ; COMPILER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA: US/10/133,065
 ; FILING DATE: 26-Apr-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA: 09/643,520
 ; FILING DATE: 22/08/2000
 ; APPLICATION NUMBER: 08/794827
 ; FILING DATE: 04-Feb-1997
 ; APPLICATION NUMBER: 08/009796
 ; FILING DATE: 05-Feb-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Evans, David W
 ; REGISTRATION NUMBER: See attached Limited Recognition under 37
 ; REFERENCE/DOCKET NUMBER: P1000R1C3
 ; TELEPHONE: 650/225-1739
 ; TELEFAX: 650/951-9891
 ; INFORMATION: SEQ ID NO 1
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 260 amino acids
 ; TYPE: Amino Acid
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-133-065-4

Query Match 99.6%; Score 1362; DB 14; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.8e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60
 DB 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60

QY 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120
 DB 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120

QY 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180
 DB 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180

QY 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240
 DB 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240

QY 241 LSDQLQAALSDHYVVEWMLK 260
 DB 241 LSDQLQAALSDHYVVEWMLK 260

RESULT 5

US-10-074-509-4
 ; Sequence 4, Application US/10074509
 ; Publication No. US20142437AI
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; TITLE OF INVENTION: HUMAN DNASE
 ; NUMBER OF SEQUENCES: 120
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER NAME: FORM:
 ; BUILDING TYPE:
 ; EQUIPMENT TYPE: 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION NUMBER: US/10/074,509
 ; FILING DATE: 11-Feb-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION NUMBER: 09/643,520
 ; FILING DATE: 22/08/2000
 ; APPLICATION NUMBER: 08/794827
 ; FILING DATE: 04-Feb-1997
 ; PUBLICATION NUMBER: 08/07996
 ; FILING DATE: 05-Feb-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnston, Sean A.
 ; ADDRESS: 10000
 ; REFERENCE/DOCKET NUMBER: P10081C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-3562
 ; TELEFAX: 650/952-9881
 ; INFORMATION:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 260 amino acids
 ; TYPE: Amino Acid
 ; ORGANISM: Homo sapiens
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-074-509-4

Query Match 99.6%; Score 1362; DB 14; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.8e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60
 DB 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60

QY 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120
 DB 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120

QY 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180
 DB 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180

QY 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240
 DB 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240

QY 241 LSDQLQAALSDHYVVEWMLK 260
 DB 241 LSDQLQAALSDHYVVEWMLK 260

RESULT 6

US-10-005-306-1
 ; Sequence 1, Application US/10005306
 ; Publication No. US20020173025AI
 ; GENERAL INFORMATION: Robert A.
 ; APPLICANT: Pan, Clark Qun
 ; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 ; FILE REFERENCE: P1042CI
 ; NUMBER OF SEQUENCES: 120
 ; CURRENT FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: US 08/663,831
 ; PRIORITY DATE: 1996-06-14
 ; NUMBER OF SEQ ID NOS: 17
 ; SEQUENCE:
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-005-306-1

Query Match 99.6%; Score 1362; DB 14; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.8e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60
 DB 1 LKTAAPNQTGFTGMSNATVSVYQLISYDIALVGVVDSHLTA VVKGLDNLNDAP 60

QY 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120
 DB 61 DTVHVSEPLGRKSKYERLYFVTPPOQVSAVSVYDDSCPCGNDTFNREPAIVRFS 120

QY 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180
 DB 121 RFTVEFAIVFLHAAPGDAVETDALYDVLVQVKGLEWLMKGFNACGSVVRFSQ 180

QY 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240
 DB 181 WSRILWTSPTFQMLPDSADTATPTPHCAVRI VVAGLLGAVVPSALPFPNFOAAG 240

QY 241 LSDQLQAALSDHYVVEWMLK 260
 DB 241 LSDQLQAALSDHYVVEWMLK 260

RESULT 7

US-10-005-306-14
 ; Sequence 14, Application US/10005306

```

; Publication No. US20020173025A1
; GENERAL INFORMATION: Robert A.
; APPLICANT: Asarachi, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; FILE REFERENCE: P1042C1
; CURRENT APPLICATION NUMBER: US/10/005,306
; PRIOR APPLICATION NUMBER: US/08/663,811
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-005-306-14

Query Match          99.6%; Score 1362; DB 14; Length 260;
Basic Local Similarity 99.6%; From 0e-14; Mismatches 0; Gaps 0;
Matches 259; Conservative 0; Mismatches 1; Indels 0;

QY 1 LKTAAPNIOFTGTSNATLVSYVQLLSHIDIALVQEVRSHTLVANGKLLNNDAP 60
DB 1 LKTAAPNIOFTGTSNATLVSYVQLLSHIDIALVQEVRSHTLVANGKLLNNDAP 60
QY 61 DTVHVVSEPLGKSTKTERLVPRQPSVDSYVDDGCFQGNTPREPAIVRFS 120
DB 61 DTVHVVSEPLGKSTKTERLVPRQPSVDSYVDDGCFQGNTPREPAIVRFS 120
QY 122 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
DB 122 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
QY 121 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
DB 121 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
QY 181 NSSILKTSPTFQWLPDSQDTATPTFCAZKIVAGKLLGAVVDSALPFPQAYG 240
DB 181 NSSILKTSPTFQWLPDSQDTATPTFCAZKIVAGKLLGAVVDSALPFPQAYG 240
QY 241 LSQDLQAQLSDHFFVEMVK 260
DB 241 LSQDLQAQLSDHFFVEMVK 260

RESULT 8
us-10-005-675-14
Sequence 14, Application US/10005675
; Publication No. US2003004403A1
; GENERAL INFORMATION: Steven
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Anti-Infective Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/10/005,675
; PRIOR APPLICATION NUMBER: US/08/663,811
; PRIOR FILING DATE: 1996-06-14
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669306
; APPLICATION DATE: 08-Dec-1999
; FILING DATE: 08-Dec-1999
; APPLICATION NUMBER: 08/6643195
; FILING DATE: 08-May-1996

```

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; APPLICATION NUMBER: 08/459909
; FILING DATE: 08-May-1996
; APPLICATION NUMBER: 08/191749
; FILING DATE: 03-Feb-1994
; APPLICATION NUMBER: 07/514,226
; FILING DATE: 13-Jul-1992
; APPLICATION NUMBER: 08/48038
; FILING DATE: 08-Dec-1993
; APPLICATION NUMBER: 07/289958
; FILING DATE: 23-Dec-1988
; ATTORNEY: A. Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: PUS30PIC10
; TELEPHONE: 650/228-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO. 14:
us-10-005-675-14

Query Match          99.6%; Score 1362; DB 15; Length 260;
Basic Local Similarity 99.6%; From 0e-14; Mismatches 0; Gaps 0;
Matches 259; Conservative 0; Mismatches 1; Indels 0;

QY 1 LKTAAPNIOFTGTSNATLVSYVQLLSHIDIALVQEVRSHTLVANGKLLNNDAP 60
DB 1 LKTAAPNIOFTGTSNATLVSYVQLLSHIDIALVQEVRSHTLVANGKLLNNDAP 60
QY 61 DTVHVVSEPLGKSTKTERLVPRQPSVDSYVDDGCFQGNTPREPAIVRFS 120
DB 61 DTVHVVSEPLGKSTKTERLVPRQPSVDSYVDDGCFQGNTPREPAIVRFS 120
QY 122 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
DB 122 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
QY 121 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
DB 121 RFEVREPAIVPELHAPGDVAIEDALDYVLDVQEGKLEDMVMDGPNAGSVRSQ 180
QY 181 NSSILKTSPTFQWLPDSQDTATPTFCAZKIVAGKLLGAVVDSALPFPQAYG 240
DB 181 NSSILKTSPTFQWLPDSQDTATPTFCAZKIVAGKLLGAVVDSALPFPQAYG 240
QY 241 LSQDLQAQLSDHFFVEMVK 260
DB 241 LSQDLQAQLSDHFFVEMVK 260

RESULT 9
us-10-012-1
Sequence 1, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Genentech
; TITLE OF INVENTION: Composites for Targeting
; CURRENT APPLICATION NUMBER: US/09/825,012
; PRIOR APPLICATION NUMBER: US/60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 282
; ORGANISM: Homo sapiens
us-09-825-012-1

Query Match          99.6%; Score 1362; DB 10; Length 282;

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Best Local Similarity 99.6%; Pred. No. 26-144; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKATATNFOGFGTSSNATSVYVQLLSYDIALVQVGRSHWANGKLLDNADAP 60
Db 2 LKATATNFOGFGTSSNATSVYVQLLSYDIALVQVGRSHWANGKLLDNADAP 82
Qy 61 DTHVTVVEEPLGRSKYERLVFVRPQVNSVNDVYDQCEFCGNTFMEPAIVRFS 120
Db 83 DTHVTVVEEPLGRSKYERLVFVRPQVNSVNDVYDQCEFCGNTFMEPAIVRFS 142
Qy 121 RFTVEFPAIVFLHARQDAVAIADLYDVLVQVKGLELWMLGDFPMACSVVRPQ 180
Db 143 RFTVEFPAIVFLHARQDAVAIADLYDVLVQVKGLELWMLGDFPMACSVVRPQ 202
Qy 181 WSSIRLWTSPTQWLIPDSAUTATPHCAIDRIVAGKLLGRGAVVPQSLPFPQAAG 240
Db 203 WSSIRLWTSPTQWLIPDSAUTATPHCAIDRIVAGKLLGRGAVVPQSLPFPQAAG 262
Qy 241 LSQQAQALSDHYPVEWLK 260
Db 263 LSQQAQALSDHYPVEWLK 282

RESULT 10

US-10-005-475-13

1 Application US/10005675

Publication No. US2003004403A1

GENERAL INFORMATION:

APPLICANT: Shk, Steven

INVENTOR: Shk, Steven; Infective Therapy

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Genentech, Inc.

CURRENT APPLICATION DATA

APPLICATION NUMBER: US/10/005,675

FILING DATE: 07-Nov-01 US2003004403A1-2001

PRIOR APPLICATION DATA: Unknown

APPLICATION NUMBER: 09/669306

FILING DATE: 25-Sep-2001

APPLICATION NUMBER: 08/97506

FILING DATE: 08-Dec-1999

APPLICATION NUMBER: 06/641395

FILING DATE: 06-May-1996

APPLICATION NUMBER: 08/459909

FILING DATE: 03-Feb-1994

APPLICATION NUMBER: 08/191749

FILING DATE: 07-May-1994

APPLICATION NUMBER: 08/137426

FILING DATE: 08-Dec-1989

APPLICATION NUMBER: 07/289958

FILING DATE: 23-Dec-1988

ATTORNEY: NAME: Johnston, Sean A.

REGISTRATION NUMBER: 35,910

REFERENCE/DOCKET NUMBER: P0530PIC10

TELEPHONE: 650/225-9582

TELEFAX: 650/225-9581

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: Amino Acid
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-005-675-13

Query Match 99.6%; Score 1162; DB 15; Length 341;

Local Similarity 99.6%; Pred. No. 2,7e-144; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKATATNFOGFGTSSNATSVYVQLLSYDIALVQVGRSHWANGKLLDNADAP 60
Db 73 LKATATNFOGFGTSSNATSVYVQLLSYDIALVQVGRSHWANGKLLDNADAP 132
Qy 61 DTHVTVVEEPLGRSKYERLVFVRPQVNSVNDVYDQCEFCGNTFMEPAIVRFS 120
Db 133 DTHVTVVEEPLGRSKYERLVFVRPQVNSVNDVYDQCEFCGNTFMEPAIVRFS 192
Qy 121 RFTVEFPAIVFLHARQDAVAIADLYDVLVQVKGLELWMLGDFPMACSVVRPQ 180
Db 193 RFTVEFPAIVFLHARQDAVAIADLYDVLVQVKGLELWMLGDFPMACSVVRPQ 252
Qy 181 WSSIRLWTSPTQWLIPDSAUTATPHCAIDRIVAGKLLGRGAVVPQSLPFPQAAG 240
Db 253 WSSIRLWTSPTQWLIPDSAUTATPHCAIDRIVAGKLLGRGAVVPQSLPFPQAAG 312
Qy 241 LSQQAQALSDHYPVEWLK 260
Db 313 LSQQAQALSDHYPVEWLK 332

RESULT 11

US-10-155-407A-1

1 Application US/10155407A

Publication No. US2003007267A1

GENERAL INFORMATION:

APPLICANT: Frenz, John

Shire, Steven J. B.

TITLE OF INVENTION: PURIFIED FORMS OF Dnaase

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/155,407A

FILING DATE: 08-Dec-1999

PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

APPLICATION NUMBER: 08/638112

FILING DATE: 11-Aug-2000

APPLICATION NUMBER: 08/442561

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: 08/634125

FILING DATE: 19-Apr-1996

APPLICATION NUMBER: 08/094631

FILING DATE: 22-Mar-1995

APPLICATION NUMBER: 08/148284

FILING DATE: 30-Nov-01 US2003007267A1-1994

APPLICATION NUMBER: 08/116186

FILING DATE: 08-Dec-1999

APPLICATION NUMBER: 07/895300

FILING DATE: 08-Jun-1992

ATTORNEY/AGENT INFORMATION:

/ FIRM: KATZ, M. NONE

/ REGISTRATION NUMBER: /

/ REFERENCE/DOCKET NUMBER: 00747C8

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 609-252-9139

/ TELEFAX: 609-252-9881

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 346 amino acids

/ TOPLOGY: Linear

/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CURRENT APPLICATION NUMBER: US/09/825,012
 CURRENT FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: US 60/237,159
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: US 0008049.9
 PRIOR FILING DATE: 2000-04-03
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1: 69
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE INFORMATION: Humanised HMG1 Pd - DNase I fusion
 US-09-825-012-76

Query Match 99.6%; Score 1362; DB 10; Length 519;
 Similarity 99.6%; Positives 144; Mismatches 1; Indels 0; Gaps 0;
 Matches 259; Conservative

QY 1 LKTAAPNIGTGTGNSNATLVSIVQLSRIDIALVQEVRSHLTAVGLLNQDAP 60
 DB 260 LKTAAPNIGTGTGNSNATLVSIVQLSRIDIALVQEVRSHLTAVGLLNQDAP 319
 QY 61 DTHVYVSEPLGMSKVERLYFVRPDQVAVSDSYVDGCEPCQNDTFNREPAIVRFS 120
 DB 320 DTHVYVSEPLGMSKVERLYFVRPDQVAVSDSYVDGCEPCQNDTFNREPAIVRFS 379
 QY 121 RFTVEVREPAIVLHAAGDVAEIDALVYLDVQEVKGLDVLKDFNAGCSYVRFSQ 180
 DB 380 RFTVEVREPAIVLHAAGDVAEIDALVYLDVQEVKGLDVLKDFNAGCSYVRFSQ 439
 QY 181 MSLRLMPTSTFQWLLPDSALTTATPTHCATDRIVVAGMLLGAUVVDSALPFFNQAAG 240
 DB 440 MSLRLMPTSTFQWLLPDSALTTATPTHCATDRIVVAGMLLGAUVVDSALPFFNQAAG 499
 QY 241 LSDQLAQAISDHPFVEMLK 260
 DB 500 LSDQLAQAISDHPFVEMLK 519

RESULT 15
 US-09-825-012-71
 Patent No. US2002012798A1
 GENERAL INFORMATION:
 TITLE OF INVENTION: Compounds for Targeting
 FILE REFERENCE: 43191-256808
 CURRENT APPLICATION NUMBER: US/09/825,012
 PRIOR APPLICATION NUMBER: US 60/237,159
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: US 0008049.9
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 71
 LENGTH: 521
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE INFORMATION: Humanised HMG1 Pd - DNase I fusion
 US-09-825-012-71

Query Match 99.6%; Score 1362; DB 10; Length 521;
 Similarity 99.6%; Positives 144; Mismatches 1; Indels 0; Gaps 0;
 Matches 259; Conservative

QY 1 LKTAAPNIGTGTGNSNATLVSIVQLSRIDIALVQEVRSHLTAVGLLNQDAP 60
 DB 262 LKTAAPNIGTGTGNSNATLVSIVQLSRIDIALVQEVRSHLTAVGLLNQDAP 321

QY 61 DTHVYVSEPLGMSKVERLYFVRPDQVAVSDSYVDGCEPCQNDTFNREPAIVRFS 120
 DB 322 DTHVYVSEPLGMSKVERLYFVRPDQVAVSDSYVDGCEPCQNDTFNREPAIVRFS 381
 QY 121 RFTVEVREPAIVLHAAGDVAEIDALVYLDVQEVKGLDVLKDFNAGCSYVRFSQ 180
 DB 382 RFTVEVREPAIVLHAAGDVAEIDALVYLDVQEVKGLDVLKDFNAGCSYVRFSQ 441
 QY 181 MSLRLMPTSTFQWLLPDSALTTATPTHCATDRIVVAGMLLGAUVVDSALPFFNQAAG 240
 DB 442 MSLRLMPTSTFQWLLPDSALTTATPTHCATDRIVVAGMLLGAUVVDSALPFFNQAAG 501
 QY 241 LSDQLAQAISDHPFVEMLK 260
 DB 502 LSDQLAQAISDHPFVEMLK 521

Search completed, November 21, 2003, 14:02:04
 Job time : 31 secs